

SCORE Search Results Details for Application 09556178 and Search Result 20101203_114247_us-09-556-178-1.rag.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101203_114247_us-09-556-178-1.rag.

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GenCore version 6.3
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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:51 ; Search time 74 Seconds
(without alignments)
9429.236 Million cell updates/sec

Title: US-09-556-178-1
Perfect score: 2898
Sequence: 1 MNVFAVKQYISKMIEDSGP.....GLHSRSKESSQVTSRSASRR 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6395994 seqs, 1224146475 residues

Total number of hits satisfying chosen parameters: 6395994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_201023:*
1: geneseqp1:*
2: geneseqp2:*
3: geneseqp3:*

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2898	100.0	570	1	AA49958	Aay49958 Human ves
2	2898	100.0	570	1	AAB03813	Aab03813 Human ves
3	2898	100.0	570	1	AAB94478	Aab94478 Human pro
4	2898	100.0	570	1	ADE61224	Ade61224 Human Pro
5	2898	100.0	570	1	ADP12603	Adp12603 Protein e
6	2898	100.0	570	1	ADR99181	Adr99181 Vacuolar
7	2898	100.0	570	2	AJF47297	Ajf47297 Human MCR
8	2898	100.0	570	3	AYE14424	Aye14424 Allograft
9	2844	98.1	570	1	ABB57217	Abb57217 Mouse isc
10	2840	98.0	570	1	ADE61222	Ade61222 Rat Prote
11	2815.5	97.2	578	1	ABG04478	Abg04478 Novel hum
12	1920	66.3	390	1	AAO21766	Aao21766 Human rib
13	1584	54.7	574	1	ABB63752	Abb63752 Drosophil
14	1584	54.7	574	2	AFB98005	Afb98005 Fruit fly

15	1310	45.2	441	1	ABG04479	Abg04479	Novel hum
16	1299.5	44.8	567	2	AQD50046	Aqd50046	Rice cDNA
17	1286	44.4	568	2	ANL98635	Anl98635	Oryza sat
18	1270	43.8	567	3	AWV44951	Awv44951	Plant pro
19	1026.5	35.4	210	1	AAAY07020	Aay07020	Breast ca
20	976	33.7	577	1	ABR53033	Abr53033	Protein s
21	976	33.7	577	1	ADK62860	Adk62860	Disease t
22	949.5	32.8	472	3	AXH20971	Axh20971	Zea mays
23	786.5	27.1	329	3	AWP61628	Awp61628	Aspergill
24	778.5	26.9	722	1	AAB18291	Aab18291	Plasmodiu
25	753	26.0	364	2	AQD41760	Aqd41760	Rice cDNA
26	714	24.6	165	1	AAO04331	Aao04331	Human pol
27	574	19.8	219	2	ARO38966	Aro38966	Soybean c
28	574	19.8	219	3	AXJ12112	Axj12112	Heteroder
29	510.5	17.6	184	2	ARO77042	Aro77042	Soybean c
30	510.5	17.6	184	3	AXJ50188	Axj50188	Heteroder
31	492	17.0	230	1	AFR53396	Afr53396	Recombina
32	492	17.0	230	3	AXD18698	Axd18698	Sorghum b
33	469.5	16.2	186	2	ARO80389	Aro80389	Soybean c
34	469.5	16.2	186	3	AXJ53535	Axj53535	Heteroder
35	416	14.4	212	3	AWP61629	Awp61629	Aspergill
36	407	14.0	621	2	ARM75723	Arm75723	Arabidops
37	407	14.0	633	1	AAG50809	Aag50809	Arabidops
38	407	14.0	633	2	ALJ97173	Alj97173	Plant pro
39	407	14.0	653	2	ARM75722	Arm75722	Arabidops
40	407	14.0	662	1	AAG50808	Aag50808	Arabidops
41	407	14.0	662	2	ALJ97172	Alj97172	Plant pro
42	401	13.8	633	1	AAG18696	Aag18696	Arabidops
43	401	13.8	633	2	ALJ52955	Alj52955	Plant pro
44	401	13.8	633	2	ARM38817	Arm38817	Arabidops
45	401	13.8	662	1	AAG18695	Aag18695	Arabidops

ALIGNMENTS

RESULT 1

AAY49958

ID AAY49958 standard; protein; 570 AA.

XX

AC AAY49958;

XX

DT 15-JUN-2007 (revised)

DT 04-FEB-2000 (first entry)

XX

DE Human vesicle trafficking protein 1.

XX

KW Human; vesicle trafficking protein; VTP-1; VTP-2; VTP-3; apoptosis;
KW cancer; inflammation; BOND_PC; vacuolar protein sorting 45A;

KW leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS54A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; GO5764;

KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.

XX

OS Homo sapiens.

XX

PN US5989859-A.
XX
PD 23-NOV-1999.
XX
PF 07-NOV-1997; 97US-00967364.
XX
PR 07-NOV-1997; 97US-00967364.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Bandman O, Guegler KJ, Corley NC, Lal P, Shah P;
XX
DR WPI; 2000-022782/02.
DR N-PSDB; AAZ35833.
DR PC:NCBI; gi18105063.
DR PC:SWISSPROT; Q9NRW7.
DR PC:BIND; 261868, 261869.
XX
PT Novel vesicle trafficking proteins used in the diagnosis, prevention, and
PT treatment of inflammation or cancer.
XX
PS Claim 9; Fig 1; 55pp; English.
XX
CC The present sequence represents the human vesicle trafficking protein
CC designated VTP-1. VTPs can be used in a method for preventing or treating
CC disease associated with an increase in apoptosis. The method can treat
CC diseases such as cancer and inflammation, by administering a VTP
CC antagonist
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVGRSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480

Db	421	KLVS	AVVEYGGKRV	RGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	G	480
Qy	481	RLKENL	YPYLGPSTL	RDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT		540
Db	481	RLKENL	YPYLGPSTL	RDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT		540
Qy	541	KSFLEE	VLASGLHSR	SKESSQVTSRSASRR		570
Db	541	KSFLEE	VLASGLHSR	SKESSQVTSRSASRR		570

RESULT 2

AAB03813

ID AAB03813 standard; protein; 570 AA.

XX

AC AAB03813;

XX

DT 15-JUN-2007 (revised)

DT 13-OCT-2000 (first entry)

XX

DE Human vesicle trafficking protein-1 (VTP-1) amino acid sequence.

XX

KW Vesicle trafficking protein; VTP-1; human; cancer; inflammation; asthma;

KW foetal development; Crohn's disease; diabetes; multiple sclerosis;

KW rheumatoid arthritis; infection; ulcerative colitis; proliferation;

KW irritable bowel syndrome; apoptosis; AIDS; Alzheimer's disease;

KW Parkinson's disease; osteoporosis; wasting disorder; BOND_PC;

KW vacuolar protein sorting 45A; leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS54A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; GO5764;

KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.

XX

OS Homo sapiens.

XX

PN US6071703-A.

XX

PD 06-JUN-2000.

XX

PF 04-AUG-1999; 99US-00368408.

XX

PR 07-NOV-1997; 97US-00967364.

XX

PA (INCY-) INCYTE PHARM INC.

XX

PI Guegler KJ, Shah P, Corley NC, Bandman O, Lal P;

XX

DR WPI; 2000-422079/36.

DR N-PSDB; AAA59873.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX

PT Identifying polynucleotides encoding vesicle trafficking proteins (VTP)

PT for treating and preventing e.g. inflammation, by detecting a

PT hybridization complex of a nucleic acid from a sample and a

PT polynucleotide encoding a VTP.
XX
PS Example; Fig 1; 55pp; English.
XX
CC This sequence represents human vesicle trafficking protein (VTP-1) amino
CC acid sequence. VTP-1 encoding cDNA was isolated from a THP-1 cell line
CC cDNA library (THP1PEB01). VTP-1 has structural and chemical homology with
CC a mouse vacuolar protein-sorting protein mVps45. The present invention
CC relates to a method for detecting human VTP encoding polynucleotide
CC sequences and includes nucleotide and protein sequences for human VTP-1,
CC VTP-2 and VTP-3. Northern analysis of VTP-1, 2, and 3 shows that their
CC expression is associated with cancer, inflammation and foetal/infant
CC development. The method of the invention is useful for screening and
CC identifying a polynucleotide encoding a human VTP, which may be used for
CC the diagnosis, prevention, or treatment of inflammation associated
CC disorder, e.g. asthma, Crohn's disease, diabetes, multiple sclerosis,
CC rheumatoid arthritis, infections, ulcerative colitis and irritable bowel
CC syndrome. Other diseases and disorders identified, prevented or treated
CC with polynucleotide sequences encoding VTP include those associated with
CC cell proliferation or apoptosis, such as AIDS, Alzheimer's disease,
CC Parkinson's disease, osteoporosis, wasting diseases and cancer
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540

Qy 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
|||||
Db 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

RESULT 3

AAB94478

ID AAB94478 standard; protein; 570 AA.

XX

AC AAB94478;

XX

DT 15-JUN-2007 (revised)

DT 26-JUN-2001 (first entry)

XX

DE Human protein sequence SEQ ID NO:15151.

XX

KW Human; primer; detection; diagnosis; antisense therapy; gene therapy;

KW BOND_PC; vacuolar protein sorting 45A;

KW leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS54A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; GO5764;

KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.

XX

OS Homo sapiens.

XX

PN EP1074617-A2.

XX

PD 07-FEB-2001.

XX

PF 28-JUL-2000; 2000EP-00116126.

XX

PR 29-JUL-1999; 99JP-00248036.

PR 27-AUG-1999; 99JP-00300253.

PR 11-JAN-2000; 2000JP-00118776.

PR 02-MAY-2000; 2000JP-00183767.

PR 09-JUN-2000; 2000JP-00241899.

XX

PA (HELI-) HELIX RES INST.

PA (REAS-) RES ASSOC FOR BIOTECHNOLOGY.

XX

PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX

DR WPI; 2001-318749/34.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX

PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-

PT length cDNAs defined in the specification, and for the detection and/or

PT diagnosis of the abnormality of the proteins encoded by the full-length

PT cDNAs.

XX

PS Claim 8; SEQ ID NO 15151; 2537pp + Sequence Listing; English.

XX

CC The present invention describes primer sets for synthesising 5602 full-

Qy 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
|||||
Db 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

RESULT 4

ADE61224

ID ADE61224 standard; protein; 570 AA.

XX

AC ADE61224;

XX

DT 15-JUN-2007 (revised)

DT 29-JAN-2004 (first entry)

XX

DE Human Protein NP_009189, SEQ ID NO 7142.

XX

KW Human; pain; neuronal tissue; gene therapy;

KW spinal segmental nerve injury; chronic constriction injury; CCI;

KW spared nerve injury; SNI; Chung; BOND_PC; vacuolar protein sorting 45A;

KW leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS54A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; GO5764;

KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.

XX

OS Homo sapiens.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; NP_009189.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX

PT New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a human protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX
SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Db	301	EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540

Db 481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
|||||

Db 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

RESULT 5

ADP12603

ID ADP12603 standard; protein; 570 AA.

XX

AC ADP12603;

XX

DT 15-JUN-2007 (revised)

DT 12-AUG-2004 (first entry)

XX

DE Protein encoded by mRNA of the invention #213.

XX

KW transplant rejection; immune system; rheumatoid arthritis; lupus;

KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS; BOND_PC;

KW vacuolar protein sorting 45A; leucocyte vacuolar protein sorting 45;

KW vacuolar protein sorting 45B (yeast);

KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;

KW VPS45B; VPS54A; VSP45A; H1VPS45;

KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a;

KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];

KW vacuolar protein sorting 45A (yeast);

KW vacuolar protein sorting 45A (yeast) [Homo sapiens];

KW vacuolar protein sorting 45 homolog (S. cerevisiae);

KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];

KW vacuolar protein sorting 45 isoform;

KW vacuolar protein sorting 45 isoform [Homo sapiens];

KW unnamed protein product; unnamed protein product [Homo sapiens]; GO5764;

KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.

XX

OS Homo sapiens.

XX

PN WO2004042346-A2.

XX

PD 21-MAY-2004.

XX

PF 24-APR-2003; 2003WO-US012946.

XX

PR 24-APR-2002; 2002US-00131831.

PR 20-DEC-2002; 2002US-00325899.

XX

PA (EXPR-) EXPRESSION DIAGNOSTICS INC.

XX

PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;

PI Rosenberg S;

XX

DR WPI; 2004-400724/37.

DR PC:NCBI; gi18105063.

DR PC:SWISSPROT; Q9NRW7.

DR PC:BIND; 261868, 261869.

XX

PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,

PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant

PT rejection, in an individual, comprises detecting the expression level of

PT the genes.

XX

PS Claim 65; SEQ ID NO 2612; 1762pp; English.

XX

CC The present invention relates to diagnosing or monitoring transplant

CC rejection, e.g. cardiac or kidney transplant rejection, in an individual

CC comprises detecting the expression level of one or more genes. The

CC methods, system and kits are useful in diagnosing or monitoring
CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
CC islet, lung, bone marrow or stem cell transplant rejection,
CC xenotransplant rejection or mechanical organ replacement rejection, in an
CC individual. The method is also useful in assessing the immune status of
CC an individual. The methods are also useful in diagnosing and monitoring
CC diseases that involve the immune system, e.g. rheumatoid arthritis,
CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
CC viral, bacterial or fungal infection. The present sequence represents a
CC protein that is encoded by the mRNA of the invention.

CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX
SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVT VVGELSRLVSERNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVT VVGELSRLVSERNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKG VSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKG VSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDH LIK	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDH LIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKES SQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKES SQVTSRSASRR	570

RESULT 6
ADR99181
ID ADR99181 standard; protein; 570 AA.
XX
AC ADR99181;
XX

DT 15-JUN-2007 (revised)
DT 02-DEC-2004 (first entry)
XX
DE Vacuolar protein sorting 45A, VSP45A, SEQ ID 187.
XX
KW Cytostatic; breast cancer; cancer; human; Vacuolar protein sorting 45A;
KW VSP45A; BOND_PC; vacuolar protein sorting 45A;
KW leucocyte vacuolar protein sorting 45;
KW vacuolar protein sorting 45B (yeast);
KW vacuolar protein sorting 45A [Homo sapiens]; VPS45A; H1; VPS45; VSP45;
KW VPS45B; VPS54A; VSP45A; H1VPS45;
KW vacuolar protein sorting 45A (yeast homolog); VPS54A, VPS45B;
KW vacuolar protein sorting 45A (yeast), isoform CRA_a;
KW vacuolar protein sorting 45A (yeast), isoform CRA_a [Homo sapiens];
KW vacuolar protein sorting 45A (yeast);
KW vacuolar protein sorting 45A (yeast) [Homo sapiens];
KW vacuolar protein sorting 45 homolog (S. cerevisiae);
KW Vacuolar protein sorting 45 homolog (S. cerevisiae) [Homo sapiens];
KW vacuolar protein sorting 45 isoform;
KW vacuolar protein sorting 45 isoform [Homo sapiens];
KW unnamed protein product; unnamed protein product [Homo sapiens]; GO5764;
KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.
XX
OS Homo sapiens.
XX
PN WO2004078035-A2.
XX
PD 16-SEP-2004.
XX
PF 27-FEB-2004; 2004WO-US007268.
XX
PR 28-FEB-2003; 2003US-0450655P.
XX
PA (FARB) BAYER PHARM CORP.
XX
PI Eveleigh D, Bigwood D;
XX
DR WPI; 2004-653556/63.
DR N-PSDB; ADR99054.
DR PC:NCBI; gi18105063.
DR PC:SWISSPROT; Q9NRW7.
DR PC:BIND; 261868, 261869.
XX
PT Diagnosing breast cancer comprises comparing the level of expression of
PT genes or gene products in a first biological sample taken from a patient
PT with that in a normal patient sample.
XX
PS Claim 3; SEQ ID NO 187; 53pp; English.
XX
CC The present invention relates to a method (M1) for diagnosing breast
CC cancer in a patient. The method comprises comparing the level of
CC expression of one or more genes or gene products in a biological sample
CC from the patient with that in a normal patient sample, where a difference
CC in the gene expression in the first sample compared to that in the second
CC sample is a diagnostic of the disease. Also claimed are: method (M2) for
CC distinguishing between normal and disease tissues; method (M3) for
CC monitoring the response of a breast cancer patient to treatment with an
CC anti-cancer agent; method (M4) for identifying a compound for treating
CC breast cancer; and an array for distinguishing between normal and disease
CC tissues comprising two or more probes corresponding to genes selected
CC from ADR98995-ADR99121 or comprising two or more polypeptides selected
CC from ADR99122-ADR99248. In M1 and M2 the genes are selected from ADR98995
CC -ADR99121 and the gene products are polypeptides selected from ADR99122-
CC ADR99248. M1 is useful for diagnosing breast cancer. M2 and the array are
CC useful for distinguishing between normal and disease tissue. M3 is useful
CC for monitoring the response of a breast cancer patient to treatment with
CC an anti-cancer agent. M4 is useful for identifying a compound for

CC treating breast cancer. Note: The sequence data for this patent did not
CC form part of the printed specification, but was obtained in electronic
CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 1; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVSASSEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLLIKG	480
Db	421	KLVSASSEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 7

AJF47297

ID AJF47297 standard; protein; 570 AA.

XX

AC AJF47297;

XX

DT 01-NOV-2007 (first entry)

XX

DE Human MCR vacuolar protein sorting 45A (VPS45A).

XX

KW Diagnosis; prognosis; prophylaxis; therapeutic; drug screening;

KW diagnostic; transgenic animal; pharmacogenetics; cancer;

KW multiple myeloma; cytostatic; melanoma; breast tumor; lung tumor;

KW colorectal tumor; prostate tumor; pancreas tumor; stomach tumor;
KW ovary tumor; bladder tumor; brain tumor; central nervous system tumor;
KW esophagus tumor; uterine cervix tumor; uterus tumor;
KW endometroid carcinoma; mouth tumor; pharynx tumor; liver tumor;
KW renal tumor; testis tumor; biliary tumor; thyroid tumor; adrenal tumor;
KW osteosarcoma; chondrosarcoma; hematological tumor; macroglobulinemia;
KW gammopathy; amyloidosis; tumor marker; BOND_PC;
KW vacuolar protein sorting 45A; leucocyte vacuolar protein sorting 45;
KW vacuolar protein sorting 45B (yeast); VPS45A; H1; VPS45; VSP45; VPS45B;
KW VPS54A; VSP45A; H1VPS45; vacuolar protein sorting 45A (yeast homolog);
KW VPS54A, VPS45B; vacuolar protein sorting 45A (yeast), isoform CRA_a;
KW vacuolar protein sorting 45A (yeast);
KW vacuolar protein sorting 45 homolog (S. cerevisiae);
KW vacuolar protein sorting 45 isoform; unnamed protein product; GO5764;
KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.
XX
OS Homo sapiens.
XX
PN WO2007095186-A2.
XX
PD 23-AUG-2007.
XX
PF 13-FEB-2007; 2007WO-US003697.
XX
PR 14-FEB-2006; 2006US-0773072P.
XX
PA (DAND) DANA FARBER CANCER INST INC.
XX
PI Depinho RA;
XX
DR WPI; 2007-701669/65.
DR N-PSDB; AJF46910.
DR REFSEQ; NP_009190.
DR PC:NCBI; gi18105063.
DR PC:SWISSPROT; Q9NRW7.
DR PC:BIND; 261868, 261869.
XX
PT Assessing whether a subject is afflicted with cancer for treating or
PT preventing cancer comprises determining an altered copy number of a
PT minimal common region (MCR) in a subject sample compared to a normal copy
PT number of the MCR.
XX
PS Disclosure; Page; 158pp; English.
XX
CC The present invention provides a method for assessing whether a subject
CC is afflicted with cancer or at risk for developing cancer. The method
CC involves comparing the copy number of a minimal common region (MCR) in a
CC subject sample to the normal copy number of the MCR, where an altered
CC copy number of the MCR in the sample and/or alterations in the amount,
CC structure and/or activity of one or more of the markers (PRKCi5, SEMA4A,
CC DHH36, GPR86 and combinations thereof) indicates that the subject is
CC afflicted with cancer or at risk for developing cancer. The invention is
CC useful for the diagnosis, prognosis, prevention and treatment of cancers
CC such as B cell cancer, multiple melanoma, myleoma, breast cancer, lung
CC cancer, bronchus cancer, colorectal cancer, prostate cancer, pancreatic
CC cancer, stomach cancer, ovarian cancer, urinary bladder cancer, brain or
CC central nervous system cancer, peripheral nervous system cancer,
CC esophageal cancer, cervical cancer, uterine or endometrial cancer, cancer
CC of the oral cavity or pharynx, liver cancer, kidney cancer, testicular
CC cancer, biliary tract cancer, small bowel or appendix cancer, salivary
CC gland cancer, thyroid gland cancer, adrenal gland cancer, osteosarcoma,
CC chondrosarcoma and cancer of hematological tissues and also Waldenstrom's
CC macroglobulinemia, heavy chain diseases (alpha chain disease, gamma chain
CC disease, mu chain disease, benign monoclonal gammopathy and immunocytic
CC amyloidosis. The invention is also useful in diagnostic assays,
CC pharmacogenomics, drug screening and in the production of transgenic
CC animals. The present sequence is a human minimal common region (MCR)

CC protein. Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC
CC Revised record issued on 18-OCT-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 2; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVSASSEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLLIKG	480
Db	421	KLVSASSEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLLIKG	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 8

AYE14424

ID AYE14424 standard; protein; 570 AA.

XX

AC AYE14424;

XX

DT 02-SEP-2010 (first entry)

XX

DE Allograft rejection diagnosis/prognosis marker protein, SEQ:2612.

XX

KW diagnostic test; gene expression; heart transplant rejection;

KW immunosuppressive; prognosis; rna quantitation; transplant rejection;

KW BOND_PC; vacuolar protein sorting 45A;

KW leucocyte vacuolar protein sorting 45;
KW vacuolar protein sorting 45B (yeast); VPS45A; H1; VPS45; VSP45; VPS45B;
KW VPS54A; VSP45A; H1VPS45; vacuolar protein sorting 45A (yeast homolog);
KW VPS54A, VPS45B; vacuolar protein sorting 45A (yeast), isoform CRA_a;
KW vacuolar protein sorting 45A (yeast);
KW vacuolar protein sorting 45 homolog (S. cerevisiae);
KW vacuolar protein sorting 45 isoform; unnamed protein product; GO5764;
KW GO5798; GO6886; GO6904; GO6954; GO16020; GO16192.
XX
OS Homo sapiens.
XX
PN US2010151467-A1.
XX
PD 17-JUN-2010.
XX
PF 08-SEP-2009; 2009US-00584615.
XX
PR 24-APR-2003; 2003WO-US012946.
PR 22-JUL-2005; 2005US-00511937.
XX
PA (XDX-) XDX INC.
XX
PI Fry K, Ly N, Morris M, Prentice J, Rosenberg S, Wohlgemuth J;
PI Woodward R;
XX
DR WPI; 2010-G86279/41.
DR PC:NCBI; gi18105063.
DR PC:SWISSPROT; Q9NRW7.
DR PC:BIND; 261868, 261869.
XX
PT Diagnosing or monitoring transplant rejection comprises detecting the
PT expression level of a nucleic acid in the patient to diagnose or monitor
PT transplant rejection in the patient.
XX
PS Example 1; SEQ ID NO 2612; 146pp; English.
XX
CC The present invention relates to a method for diagnosing or monitoring
CC transplant rejection, particularly cardiac transplant rejection in a
CC patient. The method comprises detecting the expression level of a gene
CC sequence preferably AYE11908 in a patient, by measuring the RNA level
CC expressed by the gene sequence. AYE14212-AYE14438 are proteins encoded by
CC gene expression markers AYE12145-AYE12476 for diagnosing and monitoring
CC allograft rejection.
CC
CC Revised record issued on 19-AUG-2010 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 570 AA;

Query Match 100.0%; Score 2898; DB 3; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLIGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLIGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240

Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKA FVENYPQFKKMSGTVSKHVT VVGELSRLVSE RNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKA FVENYPQFKKMSGTVSKHVT VVGELSRLVSE RNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKG VSEKYR	420
Db	361	NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKG VSEKYR	420
Qy	421	KLVS AVVEYGGKRV RGS DLFSPKDAVAITKQFLKGLKG VENVYTQHQPFLHETLDH LIKG	480
Db	421	KLVS AVVEYGGKRV RGS DLFSPKDAVAITKQFLKGLKG VENVYTQHQPFLHETLDH LIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNR TTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNR TTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEV LASGLHSRSK ESSQVTSRSASRR	570
Db	541	KSFLEEV LASGLHSRSK ESSQVTSRSASRR	570

RESULT 9

ABB57217

ID ABB57217 standard; protein; 570 AA.

XX

AC ABB57217;

XX

DT 15-JUN-2007 (revised)

DT 07-MAR-2002 (first entry)

XX

DE Mouse ischaemic condition related protein sequence SEQ ID NO:527.

XX

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;

KW vasospastic ischaemia; ischaemic condition; ischaemic disease; BOND_PC;

KW vacuolar protein sorting 45;

KW vacuolar protein sorting-associated protein 45;

KW vacuolar protein sorting protein 45;

KW vacuolar protein sorting 45 [Mus musculus]; Vps45; mVps45; AI462172;

KW AW554165; vacuolar protein sorting 45 (yeast);

KW Vacuolar protein sorting 45 (yeast) [Mus musculus];

KW vacuolar protein sorting homolog;

KW vacuolar protein sorting homolog [Mus musculus]; GO5515; GO6810; GO6904;

KW GO15031; GO16020; GO16192.

XX

OS Mus musculus.

XX

PN WO200188188-A2.

XX

PD 22-NOV-2001.

XX

PF 18-MAY-2001; 2001WO-JP004192.

XX

PR 18-MAY-2000; 2000JP-00145977.

XX

PA (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

XX

PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

XX

DR WPI; 2002-034733/04.

DR N-PSDB; ABI99530.

DR PC:NCBI; gi7305631.

DR PC:SWISSPROT; P97390.
DR PC:BIND; 261867.
XX
PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
PT expression levels of particular genes defined in the specification or by
PT determining the expression profile of a gene group comprising these
PT genes.
XX
PS Claim 2; Page 1446-1448; 2690pp; English.
XX
CC The present invention describes a method for examining ischaemic
CC conditions, comprising measuring the expression levels of particular
CC genes (I) in a test sample or determining the expression profile of a
CC gene group in the sample comprising genes selected from (I). The method
CC is useful for examining the ischaemic condition (e.g. compressive
CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
CC protein sequences in ABB57020 to ABB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
CC
CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.
XX
SQ Sequence 570 AA;

Query Match 98.1%; Score 2844; DB 1; Length 570;
Best Local Similarity 97.0%;
Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
|
Db 1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA 120
|
Db 61 EIMKHLKAICFLRPTKENVEYLIQELRRPKYSIYFYFSNVISKSDVKSLAEADEQEVVA 120

Qy 121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
|
Db 121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy 181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
|
Db 181 SEAAKRLGECVKQVISKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy 241 GINNNRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300
|
Db 241 GINNNRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKRPK 300

Qy 301 EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
|
Db 301 EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy 361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
|
Db 361 NDHSSALQNVKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR 420

Qy 421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK 480
|
Db 421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK 480

Qy 481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT 540

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      |||
Db      481 RLKENLYPYLGPSTLRDRPQDIIVFIIGGATYEEALTVYNLNRTPGVRIVLGGTTIHNT 540
      |||

Qy      541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
      |||

Db      541 KSFLEEVLASGLHSRSRESSQATRSANRR 570
      |||
```

RESULT 10

ADE61222

ID ADE61222 standard; protein; 570 AA.

XX

AC ADE61222;

XX

DT 15-JUN-2007 (revised)

DT 29-JAN-2004 (first entry)

XX

DE Rat Protein AAB53041, SEQ ID NO 7140.

XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung;

KW BOND_PC; vacuolar protein sorting 45; vesicular transport protein rvps45;

KW vacuolar protein sorting 45 [Rattus norvegicus]; Vps45; Vsp45a; MGC;

KW MGC93104; vacuolar protein sorting 45 (yeast);

KW Vacuolar protein sorting 45 (yeast) [Rattus norvegicus]; rvps45;

KW rvps45 [Rattus norvegicus]; GO5515; GO5764; GO5798; GO6886; GO6904;

KW GO6954; GO15031; GO16020; GO16192.

XX

OS Rattus norvegicus.

XX

PN WO2003016475-A2.

XX

PD 27-FEB-2003.

XX

PF 14-AUG-2002; 2002WO-US025765.

XX

PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX

PA (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX

PI Woolf C, D'urso D, Befort K, Costigan M;

XX

DR WPI; 2003-268312/26.

DR GENBANK; AAB53041.

DR PC:NCBI; gi25742604.

DR PC:SWISSPROT; O08700.

XX

PT New composition comprising two or more isolated polypeptides, useful for

PT preparing a medicament for treating pain in an animal.

XX

PS Claim 1; Page; 1017pp; English.

XX

CC The invention discloses a composition comprising two or more isolated rat

CC or human polynucleotides or a polynucleotide which represents a fragment,

CC derivative or allelic variation of the nucleic acid sequence. Also

CC claimed are a vector comprising the novel polynucleotide, a host cell

CC comprising the vector, a method for identifying a nucleotide sequence

CC which is differentially regulated in an animal subjected to pain and a

CC kit to perform the method, an array, a method for identifying an agent

CC that increases or decreases the expression of the polynucleotide sequence

CC that is differentially expressed in neuronal tissue of a first animal

CC subjected to pain, a method for identifying a compound which regulates

CC the expression of a polynucleotide sequence which is differentially

CC expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (shown in Table 2 of
CC the specification) which is differentially expressed during pain. Note:
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC information from BOND.

XX
SQ Sequence 570 AA;

Query Match 98.0%; Score 2840; DB 1; Length 570;
Best Local Similarity 97.2%;
Matches 554; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
		: :	
Db	61	EIMKHLKAICFLRPTKENVDSLIQELRRPKYSIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
		:	
Db	181	SEAAKRLGECVKQVISKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
		:	
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKRPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLQNPVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
		: : :	
Db	361	NDHSSALQNVKRLQLQNPVTEFDAARLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR	420
Qy	421	KLVSATVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Db	421	KLVSATVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
		: :	
Db	481	KLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTIHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
		:	
Db	541	KSFLEEVLASGLHSRSRESSQATRSASRR	570

RESULT 11

ABG04478

ID ABG04478 standard; protein; 578 AA.

XX

AC ABG04478;

XX

DT 13-FEB-2002 (first entry)

XX

DE Novel human diagnostic protein #4469.

XX

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX

OS Homo sapiens.

XX

PN WO200175067-A2.

XX

PD 11-OCT-2001.

XX

PF 30-MAR-2001; 2001WO-US008631.

XX

PR 31-MAR-2000; 2000US-00540217.

PR 23-AUG-2000; 2000US-00649167.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Drmanac RT, Liu C, Tang YT;

XX

DR WPI; 2001-639362/73.

DR N-PSDB; AAS68665.

XX

PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX

PS Claim 20; SEQ ID NO 34837; 103pp; English.

XX

CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX

SQ Sequence 578 AA;

Query Match 97.2%; Score 2815.5; DB 1; Length 578;

Best Local Similarity 97.7%;

Matches 558; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR 60
|||||

Db	8	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	67
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLA-EADEQEVV	119
Db	68	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVEVIGLKLIEQEVV	127
Qy	120	AEVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQL	179
Db	128	AEVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQL	187
Qy	180	SSEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHEL	239
Db	188	SSEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRLLDDAITPLLNQWTYQAMVHEL	247
Qy	240	LGINNNRIDLSRVPGISKDLREVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKP	299
Db	248	LGINNNRIDLSRVPGISKDLREVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKP	307
Qy	300	KEQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVGELSRLVSERNLLLEVSEVEQELAC	359
Db	308	KEQQKLESIGSMKAFVENYPQFKKMSGTVSKHVTTVGELSRLVSERNLLLEVSEVEQELAC	367
Qy	360	QNDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKY	419
Db	368	QNDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKY	427
Qy	420	RKLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	479
Db	428	RKLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVGNVYTQLQPFLHETLDHLIK	487
Qy	480	GRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHN	539
Db	488	GRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHN	547
Qy	540	TKSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	548	TKSFLEEVLASGLHSRSKESQVTSRSASRR	578

RESULT 12

AAO21766

ID AAO21766 standard; protein; 390 AA.

XX

AC AAO21766;

XX

DT 15-JUN-2007 (revised)

DT 13-SEP-2002 (first entry)

XX

DE Human ribosomal protein 42-9.

XX

KW Human ribosomal protein 42.9; protein metabolism disturbance disease;

KW DNA recombination; embryonic development deformity; tumour; BOND_PC;

KW vacuolar protein sorting 45A isoform;

KW vacuolar protein sorting 45A isoform [Homo sapiens]; GO5764; GO5798;

KW GO6886; GO6904; GO6954; GO16020; GO16192.

XX

OS Homo sapiens.

XX

PN CN1333254-A.

XX

PD 30-JAN-2002.

XX

PF 07-JUL-2000; 2000CN-00117043.

XX

PR 07-JUL-2000; 2000CN-00117043.

XX

PA (SHAN-) SHANGHAI BIODOOR GENE DEV CO LTD.

SCORE Search Results Details for Application 09556178 and Search Result 20101203_114247_us-09-556-178- 1.rup.

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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:52 ; Search time 347 Seconds
(without alignments)
6830.570 Million cell updates/sec

Title: US-09-556-178-1
Perfect score: 2898
Sequence: 1 MNVVFVAVKQYISKMIEDSGP.....GLHSRSKESSQVTSRSASRR 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 12869322 seqs, 4158259533 residues

Total number of hits satisfying chosen parameters: 12869322

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_201011:*
1: uniprot_sprot:*
2: uniprot_trembl:*

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2898	100.0	570	1	VPS45_HUMAN	Q9nrw7 RecName: Fu
2	2898	100.0	570	2	D3DUZ9_HUMAN	D3duz9 SubName: Fu
3	2888	99.7	570	2	Q53FR8_HUMAN	Q53fr8 SubName: Fu
4	2868	99.0	570	2	D2HBV3_AILME	D2hbv3 SubName: Fu
5	2864	98.8	570	2	A4FUX9_BOVIN	A4fux9 SubName: Fu
6	2844	98.1	570	1	VPS45_MOUSE	P97390 RecName: Fu
7	2841	98.0	570	2	Q3THX4_MOUSE	Q3thx4 SubName: Fu
8	2840	98.0	570	1	VPS45_RAT	O08700 RecName: Fu
9	2716	93.7	534	2	B7Z360_HUMAN	B7z360 SubName: Fu
10	2561	88.4	570	2	Q0D2D9_XENTR	Q0d2d9 SubName: Fu
11	2552	88.1	570	2	Q5XHB0_XENLA	Q5xhb0 SubName: Fu
12	2426	83.7	568	2	A8E7N5_DANRE	A8e7n5 SubName: Fu
13	2308	79.6	543	2	Q4TAW3_TETNG	Q4taw3 SubName: Fu
14	2244	77.4	445	2	B7Z5E4_HUMAN	B7z5e4 SubName: Fu
15	2164.5	74.7	538	2	B7Z5D4_HUMAN	B7z5d4 SubName: Fu
16	2129.5	73.5	571	2	C3Y1S4_BRAFL	C3y1s4 SubName: Fu
17	2128.5	73.4	434	2	B7Z1J7_HUMAN	B7z1j7 SubName: Fu
18	1971	68.0	568	2	A7S9U5_NEMVE	A7s9u5 SubName: Fu

19	1920	66.3	390	2	A0AR27_HUMAN	A0ar27	SubName: Fu
20	1764	60.9	377	2	Q5ZJG4_CHICK	Q5zjg4	SubName: Fu
21	1711.5	59.1	548	2	B3RRU0_TRIAD	B3rru0	SubName: Fu
22	1693.5	58.4	569	2	D7EHQ8_TRICA	D7ehq8	SubName: Fu
23	1587.5	54.8	574	2	B3NZQ1_DROER	B3nzq1	SubName: Fu
24	1584	54.7	574	2	B4PUQ8_DROYA	B4puq8	SubName: Fu
25	1584	54.7	574	2	Q9VHB5_DROME	Q9vhb5	SubName: Fu
26	1583	54.6	388	2	B5X429_SALSA	B5x429	SubName: Fu
27	1578.5	54.5	564	2	B4QWK4_DROSI	B4qwk4	SubName: Fu
28	1577.5	54.4	574	2	B4JFE0_DROGR	B4jfe0	SubName: Fu
29	1576.5	54.4	574	2	B4M4B7_DROVI	B4m4b7	SubName: Fu
30	1574	54.3	574	2	B3M2G2_DROAN	B3m2g2	SubName: Fu
31	1569	54.1	574	2	Q295J1_DROPS	Q295j1	SubName: Fu
32	1562	53.9	574	2	B4NB39_DROWI	B4nb39	SubName: Fu
33	1560	53.8	575	2	D3TNU1_GLOMM	D3tnu1	SubName: Fu
34	1556.5	53.7	574	2	B4K664_DROMO	B4k664	SubName: Fu
35	1547.5	53.4	316	2	Q5T4Q0_HUMAN	Q5t4q0	SubName: Fu
36	1533	52.9	601	2	E0VVD5_PEDHC	E0vvd5	SubName: Fu
37	1524	52.6	574	2	Q7Q285_ANOGA	Q7q285	SubName: Fu
38	1493	51.5	574	2	Q17MG1_AEDAE	Q17mg1	SubName: Fu
39	1483.5	51.2	573	2	B0WJR0_CULQU	B0wjr0	SubName: Fu
40	1469	50.7	593	2	A6RJR5_BOTFB	A6rjr5	SubName: Fu
41	1468.5	50.7	593	2	C5P291_COCP7	C5p291	SubName: Fu
42	1454.5	50.2	593	2	C4JP37_UNCRE	C4jp37	SubName: Fu
43	1449.5	50.0	549	2	B4HJY0_DROSE	B4hgy0	SubName: Fu
44	1443.5	49.8	593	2	C1GG11_PARBD	C1gg11	SubName: Fu
45	1441.5	49.7	553	2	A9UQW8_MONBE	A9uqw8	SubName: Fu

ALIGNMENTS

RESULT 1

VPS45_HUMAN

ID VPS45_HUMAN Reviewed; 570 AA.

AC Q9NRW7; Q15715; Q5T4P6; Q9Y4Z6;

DT 19-SEP-2002, integrated into UniProtKB/Swiss-Prot.

DT 01-OCT-2000, sequence version 1.

DT 02-NOV-2010, entry version 81.

DE RecName: Full=Vacuolar protein sorting-associated protein 45;

DE Short=h-VPS45;

DE Short=hlVps45;

GN Name=VPS45; Synonyms=VPS45A, VPS45B;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;

OC Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Brain;

RX MEDLINE=97149272; PubMed=8996080; DOI=10.1016/S0378-1119(96)00367-8;

RA Pevsner J., Hsu S.-C., Hyde P.S., Scheller R.H.;

RT "Mammalian homologues of yeast vacuolar protein sorting (vps) genes

RT implicated in Golgi-to-lysosome trafficking.";

RL Gene 183:7-14(1996).

RN [2]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Leukocyte;

RX MEDLINE=99332720; PubMed=10404641; DOI=10.1016/S1357-2725(99)00017-5;

RA Rajasekariah P., Eyre H.J., Stanley K.K., Walls R.S., Sutherland G.R.;

RT "Molecular cloning and characterization of a cDNA encoding the human

RT leucocyte vacuolar protein sorting (hlVps45).";

RL Int. J. Biochem. Cell Biol. 31:683-694(1999).

RN [3]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Hematopoietic stem cell;

RA Gu J., Huang Q., Yu Y., Xu S., Han Z., Fu G., Zhou J., Wang Y.,

RA Huang C., Ren S., Tu Y., Chen Z.;

RT "Novel genes expressed in hematopoietic stem/progenitor cells from

RT myelodysplastic syndrome patients.";

RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RX PubMed=14702039; DOI=10.1038/ng1285;

RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,

RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,

RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,

RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,

RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,

RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,

RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,

RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,

RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,

RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,

RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,

RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,

RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,

RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,

RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,

RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;

RT "Complete sequencing and characterization of 21,243 full-length human

RT cDNAs.";

RL Nat. Genet. 36:40-45(2004).

RN [5]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RX PubMed=16710414; DOI=10.1038/nature04727;

RA Gregory S.G., Barlow K.F., McLay K.E., Kaul R., Swarbreck D.,

RA Dunham A., Scott C.E., Howe K.L., Woodfine K., Spencer C.C.A.,

RA Jones M.C., Gillson C., Searle S., Zhou Y., Kokocinski F.,

RA McDonald L., Evans R., Phillips K., Atkinson A., Cooper R., Jones C.,

RA Hall R.E., Andrews T.D., Lloyd C., Ainscough R., Almeida J.P.,

RA Ambrose K.D., Anderson F., Andrew R.W., Ashwell R.I.S., Aubin K.,

RA Babbage A.K., Bagguley C.L., Bailey J., Beasley H., Bethel G.,

RA Bird C.P., Bray-Allen S., Brown J.Y., Brown A.J., Buckley D.,

RA Burton J., Bye J., Carder C., Chapman J.C., Clark S.Y., Clarke G.,

RA Clee C., Cobley V., Collier R.E., Corby N., Coville G.J., Davies J.,

RA Deadman R., Dunn M., Earthrowl M., Ellington A.G., Errington H.,

RA Frankish A., Frankland J., French L., Garner P., Garnett J., Gay L.,

RA Ghorri M.R.J., Gibson R., Gilby L.M., Gillett W., Glithero R.J.,

RA Grafham D.V., Griffiths C., Griffiths-Jones S., Grocock R.,

RA Hammond S., Harrison E.S.I., Hart E., Haugen E., Heath P.D.,

RA Holmes S., Holt K., Howden P.J., Hunt A.R., Hunt S.E., Hunter G.,

RA Isherwood J., James R., Johnson C., Johnson D., Joy A., Kay M.,

RA Kershaw J.K., Kibukawa M., Kimberley A.M., King A., Knights A.J.,

RA Lad H., Laird G., Lawlor S., Leongamornlert D.A., Lloyd D.M.,

RA Loveland J., Lovell J., Lush M.J., Lyne R., Martin S.,

RA Mashreghi-Mohammadi M., Matthews L., Matthews N.S.W., McLaren S.,

RA Milne S., Mistry S., Moore M.J.F., Nickerson T., O'Dell C.N.,

RA Oliver K., Palmeiri A., Palmer S.A., Parker A., Patel D., Pearce A.V.,

RA Peck A.I., Pelan S., Phelps K., Phillimore B.J., Plumb R., Rajan J.,

RA Raymond C., Rouse G., Saenphimmachak C., Sehra H.K., Sheridan E.,

RA Shownkeen R., Sims S., Skuce C.D., Smith M., Steward C.,

RA Subramanian S., Sycamore N., Tracey A., Tromans A., Van Helmond Z.,

RA Wall M., Wallis J.M., White S., Whitehead S.L., Wilkinson J.E.,

RA Willey D.L., Williams H., Wilming L., Wray P.W., Wu Z., Coulson A.,

RA Vaudin M., Sulston J.E., Durbin R.M., Hubbard T., Wooster R.,

RA Dunham I., Carter N.P., McVean G., Ross M.T., Harrow J., Olson M.V.,

RA Beck S., Rogers J., Bentley D.R.;
RT "The DNA sequence and biological annotation of human chromosome 1.";
RL Nature 441:315-321(2006).
RN [6]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Mural R.J., Istrail S., Sutton G.G., Florea L., Halpern A.L.,
RA Mobarry C.M., Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R.,
RA Flanigan M.J., Edwards N.J., Bolanos R., Fasulo D., Halldorsson B.V.,
RA Hannenhalli S., Turner R., Yooseph S., Lu F., Nusskern D.R.,
RA Shue B.C., Zheng X.H., Zhong F., Delcher A.L., Huson D.H.,
RA Kravitz S.A., Mouchard L., Reinert K., Remington K.A., Clark A.G.,
RA Waterman M.S., Eichler E.E., Adams M.D., Hunkapiller M.W., Myers E.W.,
RA Venter J.C.;
RL Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
RN [7]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Colon, and Hippocampus;
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG The MGC Project Team;
RT "The status, quality, and expansion of the NIH full-length cDNA
RT project: the Mammalian Gene Collection (MGC).";
RL Genome Res. 14:2121-2127(2004).
RN [8]
RP INTERACTION WITH ZFYVE20.
RX MEDLINE=20517446; PubMed=11062261; DOI=10.1083/jcb.151.3.601;
RA Nielsen E., Christoforidis S., Uttenweiler-Joseph S., Miaczynska M.,
RA Dewitte F., Wilm M., Hoflack B., Zerial M.;
RT "Rabenosyn-5, a novel Rab5 effector, is complexed with hVPS45 and
RT recruited to endosomes through a FYVE finger domain.";
RL J. Cell Biol. 151:601-612(2000).
RN [9]
RP INTERACTION WITH ZFYVE20.
RX PubMed=11788822; DOI=10.1038/ncb744;
RA de Renzis S., Soennichsen B., Zerial M.;
RT "Divalent Rab effectors regulate the sub-compartmental organization
RT and sorting of early endosomes.";
RL Nat. Cell Biol. 4:124-133(2002).
RN [10]
RP IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RA Colinge J., Superti-Furga G., Bennett K.L.;
RL Submitted (OCT-2008) to UniProtKB.
CC -!- FUNCTION: May play a role in vesicle-mediated protein trafficking
CC from the Golgi stack through the trans-Golgi network.
CC -!- SUBUNIT: Interacts with STX6 (By similarity). Interacts with
CC ZFYVE20.
CC -!- SUBCELLULAR LOCATION: Golgi apparatus membrane; Peripheral
CC membrane protein (By similarity). Endosome membrane; Peripheral
CC membrane protein (By similarity). Note=Associated with
CC Golgi/endosomal vesicles and the trans-Golgi network (By
CC similarity).
CC -!- TISSUE SPECIFICITY: Ubiquitous. Expression was highest in testis,
CC heart and brain, intermediate in kidney, spleen, prostate, ovary,
CC small intestine and thymus and low in lung, skeletal muscle,
CC placenta, colon, pancreas, peripheral blood leukocytes and liver.
CC -!- SIMILARITY: Belongs to the STXBP/unc-18/SEC1 family.
CC -----
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
DR EMBL; U35246; AAC50931.1; -; mRNA.
DR EMBL; AJ133421; CAB40417.1; -; mRNA.
DR EMBL; AF165513; AAF86643.1; -; mRNA.
DR EMBL; AK023170; BAB14443.1; -; mRNA.
DR EMBL; AL358073; CAI14265.1; -; Genomic_DNA.
DR EMBL; CH471121; EAW53584.1; -; Genomic_DNA.
DR EMBL; BC012932; AAH12932.1; -; mRNA.
DR EMBL; BC028382; AAH28382.1; -; mRNA.
DR IPI; IPI00090327; -.
DR PIR; JC5722; JC5722.
DR RefSeq; NP_009190.2; -.

DR UniGene; Hs.443750; -.
DR ProteinModelPortal; Q9NRW7; -.
DR SMR; Q9NRW7; 6-548.
DR STRING; Q9NRW7; -.
DR PRIDE; Q9NRW7; -.
DR Ensembl; ENST00000369130; ENSP00000358126; ENSG00000136631.
DR GeneID; 11311; -.
DR KEGG; hsa:11311; -.
DR UCSC; uc001etp.1; human.
DR CTD; 11311; -.
DR GeneCards; GC01P150039; -.
DR H-InvDB; HIX0199801; -.
DR HGNC; HGNC:14579; VPS45.
DR HPA; HPA027425; -.
DR HPA; HPA027441; -.
DR MIM; 610035; gene.
DR PharmGKB; PA37901; -.
DR HOGENOM; HBG559243; -.
DR HOVERGEN; HBG059810; -.
DR InParanoid; Q9NRW7; -.
DR OMA; GTTIHNT; -.
DR OrthoDB; EOG9PCDBM; -.
DR PhylomeDB; Q9NRW7; -.
DR NextBio; 42971; -.

Query Match 100.0%; Score 2898; DB 1; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFE	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFE	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAE	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAE	120
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCP	180
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCP	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQW	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQW	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLM	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLM	300
Qy	301	EQQKLESIA DMKAFVENYPQFKMSGTVSKHVTVVGELSRLVSE RNLL	360
Db	301	EQQKLESIA DMKAFVENYPQFKMSGTVSKHVTVVGELSRLVSE RNLL	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLR	420
Db	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFL	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFL	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIV	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIV	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 2

D3DUZ9_HUMAN

ID D3DUZ9_HUMAN Unreviewed; 570 AA.
AC D3DUZ9;
DT 23-MAR-2010, integrated into UniProtKB/TrEMBL.
DT 23-MAR-2010, sequence version 1.
DT 02-NOV-2010, entry version 8.
DE SubName: Full=Vacuolar protein sorting 45A (Yeast), isoform CRA_a;
GN Name=VPS45A; ORFNames=hCG_39383;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21108353; PubMed=11181995; DOI=10.1126/science.1058040;
RA Venter J.C., Adams M.D., Myers E.W., Li P.W., Mural R.J., Sutton G.G.,
RA Smith H.O., Yandell M., Evans C.A., Holt R.A., Gocayne J.D.,
RA Amanatides P., Ballew R.M., Huson D.H., Wortman J.R., Zhang Q.,
RA Kodira C.D., Zheng X.H., Chen L., Skupski M., Subramanian G.,
RA Thomas P.D., Zhang J., Gabor Miklos G.L., Nelson C., Broder S.,
RA Clark A.G., Nadeau J., McKusick V.A., Zinder N., Levine A.J.,
RA Roberts R.J., Simon M., Slayman C., Hunkapiller M., Bolanos R.,
RA Delcher A., Dew I., Fasulo D., Flanigan M., Florea L., Halpern A.,
RA Hannenhalli S., Kravitz S., Levy S., Mobarry C., Reinert K.,
RA Remington K., Abu-Threideh J., Beasley E., Biddick K., Bonazzi V.,
RA Brandon R., Cargill M., Chandramouliswaran I., Charlab R.,
RA Chaturvedi K., Deng Z., Di Francesco V., Dunn P., Eilbeck K.,
RA Evangelista C., Gabrielian A.E., Gan W., Ge W., Gong F., Gu Z.,
RA Guan P., Heiman T.J., Higgins M.E., Ji R.R., Ke Z., Ketchum K.A.,
RA Lai Z., Lei Y., Li Z., Li J., Liang Y., Lin X., Lu F., Merkulov G.V.,
RA Milshina N., Moore H.M., Naik A.K., Narayan V.A., Neelam B.,
RA Nusskern D., Rusch D.B., Salzberg S., Shao W., Shue B., Sun J.,
RA Wang Z., Wang A., Wang X., Wang J., Wei M., Wides R., Xiao C., Yan C.,
RA Yao A., Ye J., Zhan M., Zhang W., Zhang H., Zhao Q., Zheng L.,
RA Zhong F., Zhong W., Zhu S., Zhao S., Gilbert D., Baumhueter S.,
RA Spier G., Carter C., Cravchik A., Woodage T., Ali F., An H., Awe A.,
RA Baldwin D., Baden H., Barnstead M., Barrow I., Beeson K., Busam D.,
RA Carver A., Center A., Cheng M.L., Curry L., Danaher S., Davenport L.,
RA Desilets R., Dietz S., Dodson K., Doup L., Ferreira S., Garg N.,
RA Gluecksmann A., Hart B., Haynes J., Haynes C., Heiner C., Hladun S.,
RA Hostin D., Houck J., Howland T., Ibegwam C., Johnson J., Kalush F.,
RA Kline L., Koduru S., Love A., Mann F., May D., McCawley S.,
RA McIntosh T., McMullen I., Moy M., Moy L., Murphy B., Nelson K.,
RA Pfannkoch C., Pratt S., Puri V., Qureshi H., Reardon M.,
RA Rodriguez R., Rogers Y.H., Romblad D., Ruhfel B., Scott R., Sitter C.,
RA Smallwood M., Stewart E., Strong R., Suh E., Thomas R., Tint N.N.,
RA Tse S., Vech C., Wang G., Wetter J., Williams S., Williams M.,
RA Windsor S., Winn-Deen E., Wolfe K., Zaveri J., Zaveri K., Abril J.F.,
RA Guigo R., Campbell M.J., Sjolander K.V., Karlak B., Kejariwal A.,
RA Mi H., Lazareva B., Hatton T., Narechania A., Diemer K.,
RA Muruganujan A., Guo N., Sato S., Bafna V., Istrail S., Lippert R.,
RA Schwartz R., Walenz B., Yooseph S., Allen D., Basu A., Baxendale J.,
RA Blick L., Caminha M., Carnes-Stine J., Caulk P., Chiang Y.H.,
RA Coyne M., Dahlke C., Mays A., Dombroski M., Donnelly M., Ely D.,
RA Esparham S., Fosler C., Gire H., Glanowski S., Glasser K., Glodek A.,
RA Gorokhov M., Graham K., Gropman B., Harris M., Heil J., Henderson S.,
RA Hoover J., Jennings D., Jordan C., Jordan J., Kasha J., Kagan L.,
RA Kraft C., Levitsky A., Lewis M., Liu X., Lopez J., Ma D., Majoros W.,
RA McDaniel J., Murphy S., Newman M., Nguyen T., Nguyen N., Nodell M.,
RA Pan S., Peck J., Peterson M., Rowe W., Sanders R., Scott J.,
RA Simpson M., Smith T., Sprague A., Stockwell T., Turner R., Venter E.,
RA Wang M., Wen M., Wu D., Wu M., Xia A., Zandieh A., Zhu X.;
RT "The sequence of the human genome.";
RL Science 291:1304-1351(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Mural R.J., Istrail S., Sutton G., Florea L., Halpern A.L.,
RA Mobarry C.M., Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R.,

http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780f9eb65&ItemName=2010... 1/10/11

Qy 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
 |||
 Db 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570

RESULT 3

Q53FR8_HUMAN

ID Q53FR8_HUMAN Unreviewed; 570 AA.
 AC Q53FR8;
 DT 24-MAY-2005, integrated into UniProtKB/TrEMBL.
 DT 24-MAY-2005, sequence version 1.
 DT 05-OCT-2010, entry version 30.
 DE SubName: Full=Vacuolar protein sorting 45A variant;
 DE Flags: Fragment;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Stomach mucosa;
 RX MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
 RA Maruyama K., Sugano S.;
 RT "Oligo-capping: a simple method to replace the cap structure of
 RT eukaryotic mRNAs with oligoribonucleotides.";
 RL Gene 138:171-174(1994).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Stomach mucosa;
 RX MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
 RA Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
 RT "Construction and characterization of a full length-enriched and a 5'-
 RT end-enriched cDNA library.";
 RL Gene 200:149-156(1997).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Stomach mucosa;
 RA Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
 RA Tanaka A., Yokoyama S.;
 RL Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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 CC -----
 DR EMBL; AK223214; BAD96934.1; -; mRNA.
 DR IPI; IPI00090327; -.
 DR UniGene; Hs.443750; -.
 DR STRING; Q53FR8; -.
 DR PhosphoSite; Q53FR8; -.
 DR Ensembl; ENST00000369130; ENSP00000358126; ENSG00000136631.
 DR HGNC; HGNC:14579; VPS45.
 DR HOVERGEN; HBG059810; -.
 DR ArrayExpress; Q53FR8; -.
 DR Bgee; Q53FR8; -.
 DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.
 DR InterPro; IPR001619; Sec1-like.
 DR PANTHER; PTHR11679; Sec1-like; 1.
 DR Pfam; PF00995; Sec1; 1.
 DR SUPFAM; SSF56815; Sec1-like; 1.
 PE 2: Evidence at transcript level;
 FT NON_TER 1 1
 SQ SEQUENCE 570 AA; 65070 MW; AD7733351ECEB551 CRC64;

Query Match 99.7%; Score 2888; DB 2; Length 570;
 Best Local Similarity 99.6%;
 Matches 568; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR 60
 |||

Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLAALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRHKGVSEKYR	420
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Db	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 4

D2HBV3_AILME

ID	D2HBV3_AILME	Unreviewed;	570 AA.
AC	D2HBV3;		
DT	09-FEB-2010, integrated into UniProtKB/TrEMBL.		
DT	09-FEB-2010, sequence version 1.		
DT	05-OCT-2010, entry version 6.		
DE	SubName: Full=Putative uncharacterized protein;		
DE	Flags: Fragment;		
GN	ORFNames=PANDA_008031;		
OS	Ailuropoda melanoleuca (Giant panda).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Ursidae;		
OC	Ailuropoda.		
OX	NCBI_TaxID=9646;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RX	PubMed=20010809; DOI=10.1038/nature08696;		
RA	Li R., Fan W., Tian G., Zhu H., He L., Cai J., Huang Q., Cai Q.,		
RA	Li B., Bai Y., Zhang Z., Zhang Y., Wang W., Li J., Wei F., Li H.,		
RA	Jian M., Li J., Zhang Z., Nielsen R., Li D., Gu W., Yang Z., Xuan Z.,		
RA	Ryder O.A., Leung F.C., Zhou Y., Cao J., Sun X., Fu Y., Fang X.,		
RA	Guo X., Wang B., Hou R., Shen F., Mu B., Ni P., Lin R., Qian W.,		
RA	Wang G., Yu C., Nie W., Wang J., Wu Z., Liang H., Min J., Wu Q.,		
RA	Cheng S., Ruan J., Wang M., Shi Z., Wen M., Liu B., Ren X., Zheng H.,		
RA	Dong D., Cook K., Shan G., Zhang H., Kosiol C., Xie X., Lu Z.,		
RA	Zheng H., Li Y., Steiner C.C., Lam T.T., Lin S., Zhang Q., Li G.,		
RA	Tian J., Gong T., Liu H., Zhang D., Fang L., Ye C., Zhang J., Hu W.,		
RA	Xu A., Ren Y., Zhang G., Bruford M.W., Li Q., Ma L., Guo Y., An N.,		
RA	Hu Y., Zheng Y., Shi Y., Li Z., Liu Q., Chen Y., Zhao J., Qu N.,		
RA	Zhao S., Tian F., Wang X., Wang H., Xu L., Liu X., Vinar T., Wang Y.,		

RA Lam T.W., Yiu S.M., Liu S., Zhang H., Li D., Huang Y., Wang X.,
 RA Yang G., Jiang Z., Wang J., Qin N., Li L., Li J., Bolund L.,
 RA Kristiansen K., Wong G.K., Olson M., Zhang X., Li S., Yang H.,
 RA Wang J., Wang J.;
 RT "The sequence and de novo assembly of the giant panda genome.";
 RL Nature 463:311-317(2010).
 CC -----
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 CC Distributed under the Creative Commons Attribution-NoDerivs License
 CC -----
 DR EMBL; GL192667; EFB28489.1; -; Genomic_DNA.
 DR RefSeq; XP_002919362.1; -.
 DR GeneID; 100471437; -.
 DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.
 DR InterPro; IPR001619; Sec1-like.
 DR PANTHER; PTHR11679; Sec1-like; 1.
 DR Pfam; PF00995; Sec1; 1.
 DR SUPFAM; SSF56815; Sec1-like; 1.
 PE 4: Predicted;
 FT NON_TER 570 570
 SQ SEQUENCE 570 AA; 65066 MW; F8E11EA1E1372D39 CRC64;

Query Match 99.0%; Score 2868; DB 2; Length 570;
 Best Local Similarity 98.1%;
 Matches 559; Conservative 10; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
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Db	1	MNVVFAVKQYVSKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQREVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
		:	
Db	61	EIMKHLKAICFLRPTKENVDYLIQELRRPKYSIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
		:	
Db	121	EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
		:	
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEFQKKKPK	300
		:	
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEFQKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
		:	
Db	301	EQQKLESIADMKAFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
		:	
Db	361	NDHSSALQNVKRLQLNPKVTEFDATRLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRV RGSDFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
		:	
Db	421	KLVS AVVEYGGKRV RGSDFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
		: :	
Db	481	KLKENVYPYLGPSTLRDRPQDIIVFIIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
		:	
Db	541	KSFLEEVLASGLHSRSRESSQVTSRSASRR	570

RESULT 5
 A4FUX9_BOVIN
 ID A4FUX9_BOVIN Unreviewed; 570 AA.


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AC      A4FUX9;
DT      17-APR-2007, integrated into UniProtKB/TrEMBL.
DT      17-APR-2007, sequence version 1.
DT      05-OCT-2010, entry version 19.
DE      SubName: Full=VPS45 protein;
GN      Name=VPS45;
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC      Pecora; Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      NUCLEOTIDE SEQUENCE.
RC      STRAIN=L1 Hereford; TISSUE=Thalamus;
RA      Moore S., Alexander L., Brownstein M., Guan L., Lobo S., Meng Y.,
RA      Tanaguchi M., Wang Z., Yu J., Prange C., Schreiber K., Shenmen C.,
RA      Wagner L., Bala M., Barbazuk S., Barber S., Babakaiff R., Beland J.,
RA      Chun E., Del Rio L., Gibson S., Hanson R., Kirkpatrick R., Liu J.,
RA      Matsuo C., Mayo M., Santos R.R., Stott J., Tsai M., Wong D.,
RA      Siddiqui A., Holt R., Jones S.J., Marra M.A.;
RL      Submitted (SEP-2006) to the EMBL/GenBank/DBJ databases.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; BC123422; AAI23423.1; -; mRNA.
DR      IPI; IPI00718070; -.
DR      RefSeq; NP_001076970.1; -.
DR      UniGene; Bt.13692; -.
DR      ProteinModelPortal; A4FUX9; -.
DR      STRING; A4FUX9; -.
DR      Ensembl; ENSBTAT00000027499; ENSBTAP00000027499; ENSBTAG00000020635.
DR      GeneID; 541230; -.
DR      KEGG; bta:541230; -.
DR      CTD; 541230; -.
DR      eggNOG; maNOG05713; -.
DR      HOVERGEN; HBG059810; -.
DR      InParanoid; A4FUX9; -.
DR      PhylomeDB; A4FUX9; -.
DR      GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.
DR      InterPro; IPR001619; Sec1-like.
DR      PANTHER; PTHR11679; Sec1-like; 1.
DR      Pfam; PF00995; Sec1; 1.
DR      SUPFAM; SSF56815; Sec1-like; 1.
PE      2: Evidence at transcript level;
SQ      SEQUENCE      570 AA;   65136 MW;   7D976D91DA92A4F2 CRC64;

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Query Match          98.8%;  Score 2864;  DB 2;  Length 570;
Best Local Similarity 98.1%;
Matches 559;  Conservative 8;  Mismatches 3;  Indels 0;  Gaps 0;
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[illegible]

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Qy      361  NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR  420
      |||||:|||||
Db      361  NDHSSALQNVKRLQLNPRVTEFDAARLVMLYVLYHYERHSSNSLPGLMMDLRNKGVSEKYR  420

Qy      421  KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK  480
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Db      421  KLVSAVIEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK  480

Qy      481  RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT  540
      :|||:|||||
Db      481  KLKESLYPYLGPSTLRDRPQDIIVFIIGGATYEEALTVYNLNRTTPGVRIVLGGTMVHNT  540

Qy      541  KSFL EEVLASGLHSRSKESQVTSRSASRR  570
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Db      541  KSFL EEVLASGLHSRSKESQVTSRSASRR  570
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RESULT 6

VPS45_MOUSE

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ID      VPS45_MOUSE          Reviewed;          570 AA.
AC      P97390; Q91VK9;
DT      19-SEP-2002, integrated into UniProtKB/Swiss-Prot.
DT      01-MAY-1997, sequence version 1.
DT      05-OCT-2010, entry version 76.
DE      RecName: Full=Vacuolar protein sorting-associated protein 45;
DE      Short=mVps45;
GN      Name=Vps45; Synonyms=Vps45a;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muroidea; Muridae; Murinae; Mus; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [MRNA], AND INTERACTION WITH STX6.
RC      STRAIN=Swiss albino; TISSUE=Adipocyte;
RX      MEDLINE=97197782; PubMed=9045632; DOI=10.1074/jbc.272.10.6187;
RA      Tellam J.T., James D.E., Stevens T.H., Piper R.C.;
RT      "Identification of a mammalian Golgi Sec1p-like protein, mVps45.";
RL      J. Biol. Chem. 272:6187-6193(1997).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC      STRAIN=C57BL/6; TISSUE=Brain, and Mammary tumor;
RX      PubMed=15489334; DOI=10.1101/gr.2596504;
RG      The MGC Project Team;
RT      "The status, quality, and expansion of the NIH full-length cDNA
RT      project: the Mammalian Gene Collection (MGC).";
RL      Genome Res. 14:2121-2127(2004).
CC      -!- FUNCTION: May play a role in vesicle-mediated protein trafficking
CC      from the Golgi stack through the trans-Golgi network.
CC      -!- SUBUNIT: Interacts with ZFYVE20 (By similarity). Interacts with
CC      STX6.
CC      -!- SUBCELLULAR LOCATION: Golgi apparatus membrane; Peripheral
CC      membrane protein. Endosome membrane; Peripheral membrane protein.
CC      Note=Associated with Golgi/endosomal vesicles and the trans-Golgi
CC      network.
CC      -!- SIMILARITY: Belongs to the STXBP/unc-18/SEC1 family.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; U66865; AAB37577.1; -; mRNA.
DR      EMBL; BC012691; AAH12691.1; -; mRNA.
DR      EMBL; BC058528; AAH58528.1; -; mRNA.
DR      IPI; IPI00124291; -.
DR      RefSeq; NP_038869.1; -.
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DR UniGene; Mm.263185; -.
 DR ProteinModelPortal; P97390; -.
 DR SMR; P97390; 6-548.
 DR STRING; P97390; -.
 DR PhosphoSite; P97390; -.
 DR PRIDE; P97390; -.
 DR Ensembl; ENSMUST00000015891; ENSMUSP00000015891; ENSMUSG00000015747.
 DR GeneID; 22365; -.
 DR KEGG; mmu:22365; -.
 DR UCSC; uc008qly.1; mouse.
 DR CTD; 22365; -.
 DR MGI; MGI:891965; Vps45.
 DR eggNOG; roNOG05944; -.
 DR HOGENOM; HBG559243; -.
 DR HOVERGEN; HBG059810; -.
 DR InParanoid; P97390; -.
 DR OMA; GTTIHNT; -.
 DR OrthoDB; EOG9PCDBM; -.
 DR PhylomeDB; P97390; -.
 DR NextBio; 302685; -.
 DR ArrayExpress; P97390; -.
 DR Bgee; P97390; -.
 DR CleanEx; MM_VPS45; -.
 DR Genevestigator; P97390; -.
 DR GermOnline; ENSMUSG00000015747; Mus musculus.
 DR GO; GO:0010008; C:endosome membrane; IDA:MGI.
 DR GO; GO:0000139; C:Golgi membrane; IDA:MGI.
 DR GO; GO:0005515; F:protein binding; IPI:MGI.
 DR GO; GO:0015031; P:protein transport; IEA:UniProtKB-KW.
 DR GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.
 DR InterPro; IPR001619; Sec1-like.
 DR PANTHER; PTHR11679; Sec1-like; 1.
 DR Pfam; PF00995; Sec1; 1.
 DR SUPFAM; SSF56815; Sec1-like; 1.
 PE 1: Evidence at protein level;
 KW Endosome; Golgi apparatus; Membrane; Protein transport; Transport.
 FT CHAIN 1 570 Vacuolar protein sorting-associated
 FT protein 45.
 FT /FTId=PRO_0000206313.
 FT CONFLICT 55 55 I -> M (in Ref. 2; AAH12691).
 SQ SEQUENCE 570 AA; 65053 MW; DA704FDE8469F488 CRC64;

Query Match 98.1%; Score 2844; DB 1; Length 570;
 Best Local Similarity 97.0%;
 Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
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 Db 1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

 Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLEAEDEQEVVA 120
 |
 Db 61 EIMKHLKAICFLRPTKENVEYLIQELRRPKYSIYFIYFSNVISKSDVKSLEAEDEQEVVA 120

 Qy 121 EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
 |
 Db 121 EVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

 Qy 181 SEAAKRLAECVKQVITKEYELFEFRRTTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
 |
 Db 181 SEAAKRLGECVKQVISKEYELFEFRRTTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

 Qy 241 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300
 |
 Db 241 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKRPK 300

 Qy 301 EQQKLESIADMKAFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
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 Db 301 EQQKLESIADMKAFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360

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Qy      361 NDHSSALQNIKRLQLQPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
        |||||:||||| |||||:|||||:|||||:|||||
Db      361 NDHSSALQNVKRLQLQPKVTEFDAVRLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR 420

Qy      421 KLVS AVVEYGGKRV RGS DLFSPKDAVAITKQFLKGLKGVENVY TQHQPFLHETLDH LIKG 480
        |||||:|||||:|||||:|||||:|||||:|||||
Db      421 KLVS AVVEYGGKRV RGS DLFSPKDAVAITKQFLKGLKGVENVY TQHQPFLHETLDH LIKG 480

Qy      481 RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRITPGVRIVLGGTTVHNT 540
        |||||:|||||:|||||:|||||:|||||:|||||
Db      481 RLKENLYPYLGPSTLDRPQDIIVFIIGGATYEEALTVYNLNRITPGVRIVLGGTTIHNT 540

Qy      541 KS FLEEVLASGLHSRSKES SQVTSRSASRR 570
        |||||:||||| |||||:||
Db      541 KS FLEEVLASGLHSRSRESSQATSR SANRR 570
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RESULT 7

Q3THX4_MOUSE

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ID      Q3THX4_MOUSE          Unreviewed;          570 AA.
AC      Q3THX4;
DT      11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT      11-OCT-2005, sequence version 1.
DT      05-OCT-2010, entry version 31.
DE      SubName: Full=Putative uncharacterized protein;
GN      Name=Vps45;
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muroidea; Muridae; Murinae; Mus; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC      STRAIN=DBA/2;
RX      PubMed=16141072; DOI=10.1126/science.1112014;
RA      Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA      Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA      Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA      Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA      Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA      Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA      Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA      Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA      di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA      Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA      Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA      Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA      Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA      Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA      Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA      Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA      Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA      Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA      Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA      Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA      Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA      Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA      Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA      Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA      Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA      Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA      Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA      Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA      Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA      Grimmond S.M., Teasdale R.D., Liu E.T., Brusica V., Quackenbush J.,
RA      Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA      Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA      Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA      Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA      Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
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RA      Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA      Hayashizaki Y.;
RT      "The transcriptional landscape of the mammalian genome.";
RL      Science 309:1559-1563(2005).
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; AK146190; BAE26966.1; -; mRNA.
DR      EMBL; AK168101; BAE40072.1; -; mRNA.
DR      IPI; IPI00124291; -.
DR      UniGene; Mm.263185; -.
DR      ProteinModelPortal; Q3THX4; -.
DR      STRING; Q3THX4; -.
DR      Ensembl; ENSMUST00000015891; ENSMUSP00000015891; ENSMUSG00000015747.
DR      MGI; MGI:891965; Vps45.
DR      HOVERGEN; HBG059810; -.
DR      InParanoid; Q3THX4; -.
DR      ArrayExpress; Q3THX4; -.
DR      Bgee; Q3THX4; -.
DR      Genevestigator; Q3THX4; -.
DR      GO; GO:0010008; C:endosome membrane; IDA:MGI.
DR      GO; GO:0000139; C:Golgi membrane; IDA:MGI.
DR      GO; GO:0005515; F:protein binding; IPI:MGI.
DR      GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.
DR      InterPro; IPR001619; Sec1-like.
DR      PANTHER; PTHR11679; Sec1-like; 1.
DR      Pfam; PF00995; Sec1; 1.
DR      SUPFAM; SSF56815; Sec1-like; 1.
PE      2: Evidence at transcript level;
SQ      SEQUENCE      570 AA;  65039 MW;  DA6CBDD7967C1488 CRC64;

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Query Match 98.0%; Score 2841; DB 2; Length 570;
Best Local Similarity 96.8%;
Matches 552; Conservative 15; Mismatches 3; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVA	120
Db	61	EIMKHLKAICFLRPTKENVEYLIQELRRPKYSIYFIYFSNVISKSDVKSLAEADEQEVA	120
Qy	121	EVQEFGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLGECVKQVISKEYELFEFRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKRPK	300
Qy	301	EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Db	301	EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNVKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR	420
Qy	421	KLVS AVVEYGGKRVGRSDFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRVGRSDFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540

Db 481 RLKENLYPYLGPSTLDRPQDIIVFIIGGATYEEALTVYNLNRTTPGVRIVLGGTTIHNT 540

Qy 541 KSFLEEVLASGLHSRSKESSQVTSRSASRR 570
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Db 541 KSFLEEVLASGLHSRSRESSQATSRSANRR 570

RESULT 8

VPS45_RAT

ID VPS45_RAT Reviewed; 570 AA.

AC O08700;

DT 19-SEP-2002, integrated into UniProtKB/Swiss-Prot.

DT 01-JUL-1997, sequence version 1.

DT 05-OCT-2010, entry version 67.

DE RecName: Full=Vacuolar protein sorting-associated protein 45;

DE Short=rVps45;

GN Name=Vps45; Synonyms=Vps45a;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muroidea; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE [MRNA].

RC TISSUE=Brain;

RX MEDLINE=97260358; PubMed=9106478; DOI=10.1016/S0005-2736(97)00014-X;

RA El-Husseini A.E.-D., Guthrie H., Snutch T.P., Vincent S.R.;

RT "Molecular cloning of a mammalian homologue of the yeast vesicular

RT transport protein vps45.";

RL Biochim. Biophys. Acta 1325:8-12(1997).

RN [2]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

RC TISSUE=Heart;

RX PubMed=15489334; DOI=10.1101/gr.2596504;

RG The MGC Project Team;

RT "The status, quality, and expansion of the NIH full-length cDNA

RT project: the Mammalian Gene Collection (MGC).";

RL Genome Res. 14:2121-2127(2004).

CC -!- FUNCTION: May play a role in vesicle-mediated protein trafficking

CC from the Golgi stack through the trans-Golgi network.

CC -!- SUBUNIT: Interacts with STX6 and ZFYVE20 (By similarity).

CC -!- SUBCELLULAR LOCATION: Golgi apparatus membrane; Peripheral

CC membrane protein (By similarity). Endosome membrane; Peripheral

CC membrane protein (By similarity). Note=Associated with

CC Golgi/endosomal vesicles and the trans-Golgi network (By

CC similarity).

CC -!- TISSUE SPECIFICITY: Ubiquitous; expression was highest in testis

CC and in brain. Detected in every part of the brain.

CC -!- SIMILARITY: Belongs to the STXBP/unc-18/SEC1 family.

CC -----

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CC -----

DR EMBL; U81160; AAB53041.1; -; mRNA.

DR EMBL; BC081705; AAH81705.1; -; mRNA.

DR IPI; IPI00195452; -.

DR RefSeq; NP_742069.1; -.

DR UniGene; Rn.9316; -.

DR ProteinModelPortal; O08700; -.

DR SMR; O08700; 6-548.

DR MINT; MINT-4576687; -.

DR STRING; O08700; -.

DR PRIDE; O08700; -.

DR Ensembl; ENSRNOT00000028751; ENSRNOP00000028751; ENSRNOG00000021173.

DR GeneID; 64516; -.

DR KEGG; rno:64516; -.

DR UCSC; NM_172072; rat.

DR CTD; 64516; -.

DR RGD; 621267; Vps45.

DR eggNOG; roNOG05944; -.

```

DR      HOVERGEN; HBG059810; -.
DR      InParanoid; O08700; -.
DR      OMA; GTTIIHNT; -.
DR      OrthoDB; EOG9PCDBM; -.
DR      PhylomeDB; O08700; -.
DR      NextBio; 613314; -.
DR      ArrayExpress; O08700; -.
DR      Genevestigator; O08700; -.
DR      GermOnline; ENSRNOG00000021173; Rattus norvegicus.
DR      GO; GO:0010008; C:endosome membrane; IEA:UniProtKB-SubCell.
DR      GO; GO:0000139; C:Golgi membrane; IEA:UniProtKB-SubCell.
DR      GO; GO:0015031; P:protein transport; IEA:UniProtKB-KW.
DR      GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.
DR      InterPro; IPR001619; Sec1-like.
DR      PANTHER; PTHR11679; Sec1-like; 1.
DR      Pfam; PF00995; Sec1; 1.
DR      SUPFAM; SSF56815; Sec1-like; 1.
PE      2: Evidence at transcript level;
KW      Endosome; Golgi apparatus; Membrane; Protein transport; Transport.
FT      CHAIN             1           570           Vacuolar protein sorting-associated
FT                                     protein 45.
FT                                     /FTId=PRO_0000206314.
SQ      SEQUENCE      570 AA;   64894 MW;   0FF5E2D8E7E7E571 CRC64;

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Query Match 98.0%; Score 2840; DB 1; Length 570;
Best Local Similarity 97.2%;
Matches 554; Conservative 12; Mismatches 4; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVISMVYTQSEILQKEVYLFRIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVISMVYTQSEILQKEVYLFRIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVA	120
Db	61	EIMKHLKAICFLRPTKENVDSLIQELRRPKYSIYFIYFSNVISKSDVKSLAEADEQEVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLGECVKQVISKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKRPK	300
Qy	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Db	301	EQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNVKRLQLQNPKVTEFDAVRLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALT VYNLNRTPGVRIVLGGTTVHNT	540
Db	481	KLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALT VYNLNRTPGVRIVLGGTTIHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSRESSQATSRSASRR	570

RESULT 9

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B7Z360_HUMAN
ID   B7Z360_HUMAN                      Unreviewed;       534 AA.
AC   B7Z360;
DT   03-MAR-2009, integrated into UniProtKB/TrEMBL.
DT   03-MAR-2009, sequence version 1.
DT   05-OCT-2010, entry version 11.
DE   SubName: Full=cDNA FLJ54353, highly similar to Vacuolar protein sorting-associated protein 45;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Hippocampus;
RA   Wakamatsu A., Yamamoto J., Kimura K., Ishii S., Watanabe K.,
RA   Sugiyama A., Murakawa K., Kaida T., Tsuchiya K., Fukuzumi Y.,
RA   Kumagai A., Oishi Y., Yamamoto S., Ono Y., Komori Y., Yamazaki M.,
RA   Kisu Y., Nishikawa T., Sugano S., Nomura N., Isogai T.;
RT   "NEDO human cDNA sequencing project focused on splicing variants.";
RL   Submitted (OCT-2007) to the EMBL/GenBank/DDBJ databases.
CC   -----
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   -----
DR   EMBL; AK295529; BAH12096.1; -; mRNA.
DR   IPI; IPI00090327; -.
DR   UniGene; Hs.443750; -.
DR   Ensembl; ENST00000369130; ENSP00000358126; ENSG00000136631.
DR   HGNC; HGNC:14579; VPS45.
DR   HOVERGEN; HBG059810; -.
DR   Bgee; B7Z360; -.
DR   GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.
DR   InterPro; IPR001619; Sec1-like.
DR   PANTHER; PTHR11679; Sec1-like; 1.
DR   Pfam; PF00995; Sec1; 1.
DR   SUPFAM; SSF56815; Sec1-like; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   534 AA;   61107 MW;   8FC6896E27D62D59 CRC64;
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Query Match 93.7%; Score 2716; DB 2; Length 534;
Best Local Similarity 99.8%;
Matches 533; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	37	MVYQTQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI	96
Db	1	MVYQTQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI	96
Qy	97	YFSNVISKSDVKSLAEADEQEVVAEVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLS	156
Db	61	YFSNVISKSDVKSLAEADEQEVVAEVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLS	120
Qy	157	RTTQGLTALLLSLKKCPMIRYQLSSEAAKRLAECVKQVITKEYELFEFRRTVEPPLLLIL	216
Db	121	RTTQGLTALLLSLKKCPMIRYQLSSEAAKRLAECVKQVITKEYELFEFRRTVEPPLLLIL	180
Qy	217	DRCDDAITPLLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNM	276
Db	181	DRCDDAITPLLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNM	240
Qy	277	YLNFAEIGSNIKNLMEDFQKKKPKEQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVG	336
Db	241	YLNFAEIGSNIKNLMEDFQKKKPKEQQKLESIA DMKAFVESYPQFKKMSGTVSKHVTVVG	300
Qy	337	ELSRVLVSERNLLEVSEVEQELACQNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYE	396
Db	301	ELSRVLVSERNLLEVSEVEQELACQNDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYE	360
Qy	397	RHSSNSLPGLMMDLRNKGVSEKYRKLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGL	456


```
Db          361 RHSSNSLPGLMMDLRNKGVSEKYRKLVS AVVEYGGKRVGSDLFSPKDAVAITKQFLKGL 420

Qy          457 KGVENVYTQHQPFLHETLDHLIKGRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEAL 516
          |||
Db          421 KGVENVYTQHQPFLHETLDHLIKGRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEAL 480

Qy          517 TVYNLNRTPGVRIVLGGTTVHNKTSFLEEVLASGLHSRSKESQVTSRSASRR 570
          |||
Db          481 TVYNLNRTPGVRIVLGGTTVHNKTSFLEEVLASGLHSRSKESQVTSRSASRR 534
```

RESULT 10

Q0D2D9_XENTR

```
ID      Q0D2D9_XENTR          Unreviewed;          570 AA.
AC      Q0D2D9;
DT      17-OCT-2006, integrated into UniProtKB/TrEMBL.
DT      17-OCT-2006, sequence version 1.
DT      05-OCT-2010, entry version 19.
DE      SubName: Full=Vacuolar protein sorting 45A;
GN      Name=vps45;
OS      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC      Xenopodinae; Xenopus; Silurana.
OX      NCBI_TaxID=8364;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC      TISSUE=Testes;
RG      NIH - Xenopus Gene Collection (XGC) project;
RL      Submitted (AUG-2006) to the EMBL/GenBank/DDBJ databases.
CC      -----
CC      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC      Distributed under the Creative Commons Attribution-NoDerivs License
CC      -----
DR      EMBL; BC121938; AAI21939.1; -; mRNA.
DR      RefSeq; NP_001072504.1; -.
DR      UniGene; Str.52455; -.
DR      ProteinModelPortal; Q0D2D9; -.
DR      SMR; Q0D2D9; 7-553.
DR      GeneID; 779959; -.
DR      KEGG; xtr:779959; -.
DR      CTD; 779959; -.
DR      Xenbase; XB-GENE-961682; vps45.
DR      eggNOG; veNOG10291; -.
DR      HOVERGEN; HBG059810; -.
DR      GO; GO:0006904; P:vesicle docking involved in exocytosis; IEA:InterPro.
DR      InterPro; IPR001619; Sec1-like.
DR      PANTHER; PTHR11679; Sec1-like; 1.
DR      Pfam; PF00995; Sec1; 1.
DR      SUPFAM; SSF56815; Sec1-like; 1.
PE      2: Evidence at transcript level;
SQ      SEQUENCE 570 AA; 65048 MW; 722B3FF9BCE6B497 CRC64;
```

```
Query Match          88.4%;  Score 2561;  DB 2;  Length 570;
Best Local Similarity 87.2%;
Matches 497;  Conservative 36;  Mismatches 37;  Indels 0;  Gaps 0;
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Qy          1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
          |||
Db          1 MNVVLAVKQYVSKMIEDSGPGMKVLLMDKETTSVSMVYTQSEILQKEVYLFERIDSTNR 60

Qy          61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
          | |||
Db          61 ESMKHLKAICFLRPTKENVEYLIKELRRPKYSVYFLYFSNVISKSDVKSLAEADEQEVVA 120

Qy          121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
          |||
Db          121 EVQEFYGDYIAVNPHVFSNLIVGCGYQGRNWDVHLYRTTQGLTALLSLKKCPMIRYQLS 180

Qy          181 SEAAKRLAECVKQVITKEYELFEFRRTTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
```

SCORE Search Results Details for Application 09556178

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101203_114247_us-09-556-178-1.rpr.

GenCore version 6.3
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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:52 ; Search time 10 Seconds
(without alignments)
5484.355 Million cell updates/secTitle: US-09-556-178-1
Perfect score: 2898
Sequence: 1 MNVFAVKQYISKMIEDSGP.....GLHSRSKESQVTSRSASRR 570Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summariesDatabase : PIR_80:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2833	97.8	570	2 JC5722	vacuolar protein s
2	1299	44.8	569	2 T52056	vacuolar protein s
3	1296	44.7	569	2 T00445	vacuolar protein-s
4	1207.5	41.7	547	2 T29567	hypothetical prote
5	1137.5	39.3	558	2 S62458	vacuolar protein s
6	976	33.7	577	2 S48542	VPS45 protein - ye
7	778.5	26.9	722	2 D71607	VPS45-like protein
8	386.5	13.3	593	2 A55931	mu Sec1 protein -
9	382	13.2	648	2 JC4674	Sly1 protein - rat
10	376.5	13.0	594	2 A57022	Munc18-2 - rat
11	372.5	12.9	635	2 T06619	hypothetical prote
12	366	12.6	639	2 T41585	stxbp-unc-18-sec1
13	361	12.5	673	2 S36747	probable acetylcho
14	355	12.2	592	2 I49239	vesicle transport
15	349.5	12.1	666	2 A39610	SLY1 protein - yea
16	344.5	11.9	597	2 S33578	rop protein - frui
17	339	11.7	733	2 C86258	protein F5011.8 [i
18	338.5	11.7	693	2 T41443	syntaxin-binding p
19	333.5	11.5	594	2 S39345	unc-18 protein hom
20	332.5	11.5	594	2 A53455	syntaxin-binding p
21	331.5	11.4	707	2 T22127	hypothetical prote
22	325.5	11.2	594	2 S39346	unc-18 protein hom
23	315.5	10.9	562	2 T32581	hypothetical prote
24	297	10.2	627	2 G84558	probable SEC1 fami
25	235	8.1	724	2 S17479	SEC1 protein - yea
26	207.5	7.2	601	2 JC5720	vacuolar protein s
27	197.5	6.8	592	2 T50328	probable vacuolar
28	168	5.8	576	2 S27790	SLP1 protein homol
29	163	5.6	691	2 A34708	vacuolar protein-s
30	162.5	5.6	535	2 T06734	vacuolar protein s
31	159.5	5.5	617	2 JC5721	vacuolar protein s
32	142	4.9	1005	2 A64465	hypothetical prote
33	142	4.9	1837	2 T41023	probable nuclear p
34	135	4.7	662	2 AG2420	hypothetical prote
35	134.5	4.6	1188	2 F64367	pyruvate, water di
36	133	4.6	944	1 S48821	probable membrane
37	132.5	4.6	1169	2 A64505	Pl15 homolog - Met
38	132.5	4.6	3225	2 I52300	giantin - human
39	132.5	4.6	3259	1 A56539	giantin - human
40	132	4.6	554	2 E90601	hypothetical prote
41	132	4.6	864	2 B90395	purine NTPase [imp
42	132	4.6	1330	2 H89567	protein T08A9.1 [i
43	132	4.6	1679	2 S48385	hypothetical prote
44	131.5	4.5	886	2 H69378	conserved hypothet
45	131	4.5	833	2 H72205	maltose ABC transp

ALIGNMENTS

RESULT 1
JC5722
vacuolar protein sorting protein 45 - human
C;Species: Homo sapiens (man)
C;Date: 09-Dec-1997 #sequence_revision 09-Dec-1997 #text_change 09-Jul-2004
C;Accession: JC5722
R;Pevsner, J.; Hsu, S.C.; Hyde, P.S.; Scheller, R.H.
Gene 183, 7-14, 1996
A;Title: Mammalian homologues of yeast vacuolar protein sorting (vps) genes implicated in Golgi-to-lysosome trafficking.
A;Reference number: JC5720; MUID:97149272; PMID:8996080
A;Accession: JC5722
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA

A;Residues: 1-570 <PEV>
A;Cross-references: UNIPROT:Q9NRW7; UNIPARC:UPI000016B178; GB:U35246; NID:g1477465; PIDN:AAC50931.1; PID:g1477466
A;Experimental source: brain
C;Comment: This protein is involved in vasicular trafficking between the Golgi and lysosome.
C;Superfamily: vacuolar protein sorting protein VPS45

Query Match 97.8%; Score 2833; DB 2; Length 570;
Best Local Similarity 97.0%;
Matches 553; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MNVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
Db 1 MNVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
Qy 61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVA 120
Db 61 EIMKHLKAICFLRPTKENVDSLIQELRRPKYSIYFIYFSNVISKSDVKSLAEADEQEVA 120
Qy 121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
Db 121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
Qy 181 SEAAKRLAECVKQVITKEYELFEFRRTVPPLLLILDRCDDAITPLNQWTYQAMVHELL 240
Db 181 SEAAKRLGECVKQVISKEYELFEFRRTVPPLLLILDRCDDAITPLNQWTYQAMVHELL 240
Qy 241 GINNRRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFABEIGSNIKNLMEDFQKKKPK 300
Db 241 DINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFABEIGSNIKNLMEDFQKKRPK 300
Qy 301 EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
Db 301 EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
Qy 361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
Db 361 NDHSSALQNVKRLQNPKVTEFDAVRLVMLYALHYERHSSNSLPGLITVDRSKGVAEKYR 420
Qy 421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480
Db 421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480
Qy 481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGTTVHNT 540
Db 481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGTTIHNT 540
Qy 541 KSFLEEVLASGLHSRSKESQVTSRSASRR 570
Db 541 KSFLEEVLASGLHSRSRESSQATRSASRR 570

RESULT 2
T52056
vacuolar protein sorting protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T52056
R;Bassham, D.C.; Raikhel, N.V.
Plant Physiol. 117, 407-415, 1998
A;Title: An Arabidopsis VPS45p homolog implicated in protein transport to the vacuole.
A;Reference number: Z25924; MUID:98289086; PMID:9625693
A;Accession: T52056
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-569 <BAS>
A;Cross-references: UNIPROT:O49048; UNIPARC:UPI000016D924; EMBL:AF036234; PIDN:AAC39472.1
C;Genetics:
A;Note: VPS45
C;Superfamily: vacuolar protein sorting protein VPS45

Query Match 44.8%; Score 1299; DB 2; Length 569;
Best Local Similarity 45.3%;
Matches 266; Conservative 124; Mismatches 157; Indels 40; Gaps 12;

Qy 1 MNVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERID--SQ 58
Db 1 MVLVTSVRDYINRMLQDIS-GMKVLILDSETVSNVSIVYSQSELLQKEVFLVEMIDISIV 59
Qy 59 NREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEV 118
Db 60 SKESMSHLKAVYFIRPTSDNIQKLRYQLANPRFGEYHLFFSNLLKDTQIHILADSDEQEV 119
Qy 119 VAEVQEFYGDYIAVNPHLFSNLILGCCQGRNW-----DPAQL----SRTTQGLTALL 166
Db 120 VQQVQEYYADFVSGDPYHFTLNM----ASNHYMIPAVVDPSGLQRFSDRVVDGIAAVF 174
Qy 167 LSLKKCPMIRYQLSSEAAKRLA-ECVKQVITKEYELFEFRRTVPPLLLILDRCDDAITP 225
Db 175 LALKRRPVIRYQRTSDTAKRIAHE TAKLMYQHESALFDFRRTSSPLLLVIDRRDDPVTP 234
Qy 226 LLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLR-EVVLSAENDEFYANNMYLNFABEIG 284
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Qy 285 SNIKLMEDFQKKKPKQKQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSE 344
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Qy 345 RNLLEVSEVEQELACQNDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLP 404
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Qy 405 GLMMDLRNK--GVSEKYRK-LVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVEN 461
Db 410 VQLMQLFNKLASRSPKYKPLGVQFLKQAGVEKRTGDLFGNRDLLNIARNMARGLKGVEN 469
Qy 462 VYTQHQPFLHETLDHLIKGRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNL 521
Db 470 VYTQHQPFLFQTME SITRGLRDVDYFPVGDHFQQGRPQEVVIFMVGTTTYEESRVALQ 529
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Db 522 NRTTPGVRIVLGTTVHNTKSFLEEVLASGLHSRSKESQVTSRSAS 568

SCORE Search Results Details for Application 09556178 and Search Result 20101203_114248_us-09-556-178-1.ra1.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101203_114248_us-09-556-178-1.ra1.

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GenCore version 6.3
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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:52 ; Search time 57 Seconds
(without alignments)
3961.810 Million cell updates/sec

Title: US-09-556-178-1
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2170800 seqs, 396181022 residues

Total number of hits satisfying chosen parameters: 2170800

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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SUMMARIES

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		Match	Length			
1	2898	100.0	570	1	US-08-967-364-1	Sequence 1, Appli
2	2898	100.0	570	2	US-09-368-408-1	Sequence 1, Appli
3	2898	100.0	570	3	US-10-511-937-2612	Sequence 2612, Ap
4	2898	100.0	570	3	US-11-443-428A-738990	Sequence 738990,
5	2898	100.0	570	3	US-11-443-428A-738993	Sequence 738993,
6	2898	100.0	570	3	US-11-443-428A-738994	Sequence 738994,
7	2898	100.0	570	3	US-11-443-428A-739003	Sequence 739003,
8	2844	98.1	570	1	US-08-967-364-7	Sequence 7, Appli
9	2844	98.1	570	2	US-09-368-408-7	Sequence 7, Appli
10	2783	96.0	552	3	US-11-443-428A-738991	Sequence 738991,

11	2777	95.8	552	3	US-11-443-428A-738998	Sequence 738998,
12	2769	95.5	612	3	US-11-443-428A-739002	Sequence 739002,
13	2721	93.9	534	3	US-11-443-428A-738992	Sequence 738992,
14	2721	93.9	534	3	US-11-443-428A-739001	Sequence 739001,
15	2550	88.0	526	3	US-11-443-428A-739004	Sequence 739004,
16	1873	64.6	372	3	US-11-443-428A-738999	Sequence 738999,
17	1755	60.6	359	3	US-11-443-428A-738995	Sequence 738995,
18	1273	43.9	567	3	US-11-241-607-62939	Sequence 62939, A
19	976	33.7	577	2	US-09-487-558B-420	Sequence 420, App
20	917	31.6	398	3	US-10-703-032-125739	Sequence 125739,
21	788	27.2	162	3	US-11-443-428A-739006	Sequence 739006,
22	786.5	27.1	329	3	US-09-417-507-33074	Sequence 33074, A
23	757.5	26.1	200	3	US-11-443-428A-738996	Sequence 738996,
24	744	25.7	158	3	US-11-443-428A-739005	Sequence 739005,
25	613	21.2	129	3	US-11-443-428A-739000	Sequence 739000,
26	492	17.0	230	3	US-10-767-701-43244	Sequence 43244, A
27	416	14.4	212	3	US-09-417-507-33075	Sequence 33075, A
28	386.5	13.3	593	1	US-08-900-927-3	Sequence 3, Appli
29	386.5	13.3	593	1	US-09-191-279-3	Sequence 3, Appli
30	386.5	13.3	593	2	US-09-334-476-3	Sequence 3, Appli
31	384	13.3	95	3	US-11-443-428A-738997	Sequence 738997,
32	383	13.2	628	3	US-11-443-428A-893746	Sequence 893746,
33	383	13.2	633	3	US-11-443-428A-893756	Sequence 893756,
34	382.5	13.2	593	1	US-08-900-927-1	Sequence 1, Appli
35	382.5	13.2	593	1	US-09-191-279-1	Sequence 1, Appli
36	382.5	13.2	593	2	US-09-334-476-1	Sequence 1, Appli
37	382.5	13.2	593	3	US-11-483-373B-2	Sequence 2, Appli
38	382.5	13.2	609	3	US-11-443-428A-857469	Sequence 857469,
39	380.5	13.1	632	3	US-11-443-428A-893751	Sequence 893751,
40	380	13.1	617	3	US-11-443-428A-893748	Sequence 893748,
41	380	13.1	648	3	US-11-443-428A-893749	Sequence 893749,
42	380	13.1	651	3	US-11-443-428A-893754	Sequence 893754,
43	380	13.1	651	3	US-11-443-428A-893758	Sequence 893758,
44	378	13.0	644	3	US-11-443-428A-857458	Sequence 857458,
45	372	12.8	619	3	US-11-443-428A-857474	Sequence 857474,

ALIGNMENTS

RESULT 1

US-08-967-364-1

; Sequence 1, Application US/08967364

; Patent No. 5989859

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Lal, Preeti

; APPLICANT: Guegler, Karl J.

; APPLICANT: Shah, Purvi

; APPLICANT: Corley, Neil C.

; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Dr.

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/967,364

; FILING DATE: No. 5989859ember 7, 1997

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPIPEB01
; CLONE: 75871
US-08-967-364-1
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Query Match          100.0%; Score 2898; DB 1; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVA 120
        |
Db     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVA 120

Qy    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180
        |
Db    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180

Qy    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
        |
Db    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300
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Db    241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300

Qy    301 EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
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Qy    361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
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RESULT 2

US-09-368-408-1
; Sequence 1, Application US/09368408
; Patent No. 6071703
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/368,408
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/967,364
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C.
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0417 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 570 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPIPEB01
; CLONE: 75871
US-09-368-408-1

Query Match 100.0%; Score 2898; DB 2; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
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Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
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Qy	241	GINNNRIDLSRVPGISKDLREVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
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Qy	361	NDHSSALQNIKRLQNPQVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSSEKYR	420
Db	361	NDHSSALQNIKRLQNPQVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSSEKYR	420
Qy	421	KLVSAAVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFLLHETLDHLIKG	480
Db	421	KLVSAAVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTOHQPFLLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
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RESULT 3

US-10-511-937-2612

; Sequence 2612, Application US/10511937

; Patent No. 7691569

; GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

; FILE REFERENCE: 506612000104

; CURRENT APPLICATION NUMBER: US/10/511,937

; CURRENT FILING DATE: 2004-10-19

; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2003-04-24

; PRIOR APPLICATION NUMBER: US 10/131,831

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: US 10/325,899

; PRIOR FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 3117

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2612

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-511-937-2612

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Best Local Similarity 100.0%;

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Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
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Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVT VVGELSRLVSEERNLLEVSEVEQELACQ	360
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Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
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RESULT 4

US-11-443-428A-738990

; Sequence 738990, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738990

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738990

Query Match 100.0%; Score 2898; DB 3; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLDRPDIIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLDRPDIIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 5

US-11-443-428A-738993

; Sequence 738993, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738993

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738993

Query Match 100.0%; Score 2898; DB 3; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 6

US-11-443-428A-738994

; Sequence 738994, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738994
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738994

Query Match 100.0%; Score 2898; DB 3; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570

RESULT 7

US-11-443-428A-739003
; Sequence 739003, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen

```
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 739003
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-739003
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Query Match          100.0%; Score 2898; DB 3; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
        |
Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
        |
Db     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120

Qy    121 EVQEFYGYDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
        |
Db    121 EVQEFYGYDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
        |
Db    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 300
        |
Db    241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKPK 300

Qy    301 EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
        |
Db    301 EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy    361 NDHSSALQNIKRLQNPKEVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSSEKYR 420
        |
Db    361 NDHSSALQNIKRLQNPKEVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSSEKYR 420

Qy    421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLLIKG 480
        |
Db    421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLLIKG 480

Qy    481 RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
        |
Db    481 RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy    541 KSFLKEEVLASGLHSRSKESQVTSRSASRR 570
        |
Db    541 KSFLKEEVLASGLHSRSKESQVTSRSASRR 570
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RESULT 8

US-08-967-364-7

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; Sequence 7, Application US/08967364
; Patent No. 5989859
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Guegler, Karl J.
```

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; APPLICANT:  Shah, Purvi
; APPLICANT:  Corley, Neil C.
; TITLE OF INVENTION:  VESICLE TRAFFICKING PROTEINS
; NUMBER OF SEQUENCES:  9
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;   STREET:  3174 Porter Dr.
;   CITY:  Palo Alto
;   STATE:  CA
;   COUNTRY:  USA
;   ZIP:  94304
; COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Diskette
;   COMPUTER:  IBM Compatible
;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/967,364
;   FILING DATE:  No. 5989859ember 7, 1997
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
; ATTORNEY/AGENT INFORMATION:
;   NAME:  Cerrone, Michael C.
;   REGISTRATION NUMBER:  39,132
;   REFERENCE/DOCKET NUMBER:  PF-0417 US
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  650-855-0555
;   TELEFAX:  650-845-4166
; INFORMATION FOR SEQ ID NO:  7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH:  570 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
; IMMEDIATE SOURCE:
;   LIBRARY:  GenBank
;   CLONE:  GI7703494
US-08-967-364-7
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Query Match          98.1%;  Score 2844;  DB 1;  Length 570;
Best Local Similarity 97.0%;
Matches 553;  Conservative 14;  Mismatches 3;  Indels 0;  Gaps 0;
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Qy      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
        |||
Db      1  MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
        |||:|
Db     61  EIMKHLKAICFLRPTKENVEYLIQELRRPKYSIYFIYFSNVISKSDVKSLAEADEQEVVA 120

Qy    121  EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
        |||
Db    121  EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy    181  SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
        |||:|
Db    181  SEAAKRLGECVKQVISKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241  GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK 300
        |||:|
Db    241  GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKRPK 300

Qy    301  EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
        |||
Db    301  EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
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Qy	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNVKRLQLQNPKVTEFDAVRLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR	420
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLDRPQDIIVFIIGGATYEEALTVYNLNRTTPGVRIVLGGTTIHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSRESSQATSRSANRR	570

RESULT 9
 US-09-368-408-7
 ; Sequence 7, Application US/09368408
 ; Patent No. 6071703
 ; GENERAL INFORMATION:
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Shah, Purvi
 ; APPLICANT: Corley, Neil C.
 ; TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Dr.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/368,408
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/967,364
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cerrone, Michael C.
 ; REGISTRATION NUMBER: 39,132
 ; REFERENCE/DOCKET NUMBER: PF-0417 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 570 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: GenBank
 ; CLONE: GI7703494
 US-09-368-408-7

Query Match
 98.1%;
 Score 2844;
 DB 2;
 Length 570;

Best Local Similarity 97.0%;

Matches 553; Conservative 14; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MNVVFQYISKMIEDSGPGMKVLLMDKETTGIQSEILQKEVYLFERIDSQNR 60
      |
Db      1 MNVVFQYISKMIEDSGPGMKVLLMDKETTGIQSEILQKEVYLFERIDSQNR 60

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
      |
Db     61 EIMKHLKAICFLRPTKENVEYLIQELRRPKYSIYFIYFSNVISKSDVKSLAEADEQEVVA 120

Qy    121 EVQEFYGDYIAVNPHLFSNLIGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
      |
Db    121 EVQEFYGDYIAVNPHLFSNLIGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy    181 SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
      |
Db    181 SEAAKRLGECVKQVISKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241 GINNNRIDLSRVPGISKDLREVLVSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300
      |
Db    241 GINNNRIDLSRVPGISKDLREVLVSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKRPK 300

Qy    301 EQQKLESIAADMKAQFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
      |
Db    301 EQQKLESIAADMKAQFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy    361 NDHSSALQNIKRLQNPQVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSSEKYR 420
      |
Db    361 NDHSSALQNVKRLQNPQVTEFDAARLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR 420

Qy    421 KLVSQVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480
      |
Db    421 KLVSQVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIKG 480

Qy    481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT 540
      |
Db    481 RLKENLYPYLGPSTLRDRPQDIIVFIIGGATYEEALTVYNLNRTTPGVRIVLGGTTIHNT 540

Qy    541 KSFLEEVLASGLHSRSKESQVTSRSASRR 570
      |
Db    541 KSFLEEVLASGLHSRSRESSQATSRSANRR 570
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RESULT 10

US-11-443-428A-738991

; Sequence 738991, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738991

; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738991

Query Match 96.0%; Score 2783; DB 3; Length 552;
Best Local Similarity 96.8%;
Matches 552; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQ--	58
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	59	-----ENVVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	102
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	103	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	162
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	163	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	222
Qy	241	GINNNRIDLSRVPGISKDLREVLVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	223	GINNNRIDLSRVPGISKDLREVLVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	282
Qy	301	EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	283	EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	342
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	343	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	402
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	403	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	462
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	463	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	522
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	523	KSFLEEVLASGLHSRSKESQVTSRSASRR	552

RESULT 11

US-11-443-428A-738998

; Sequence 738998, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738998
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738998

Query Match 95.8%; Score 2777; DB 3; Length 552;
Best Local Similarity 99.3%;
Matches 547; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVSATVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVSATVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KS--FLEEVLA	549
Db	541	KSKRFLREGLA	551

RESULT 12
US-11-443-428A-739002
; Sequence 739002, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili

```
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 739002
; LENGTH: 612
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-739002
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Query Match          95.5%; Score 2769; DB 3; Length 612;
Best Local Similarity 96.5%;
Matches 546; Conservative 5; Mismatches 11; Indels 4; Gaps 1;
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Qy      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
      |
Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
      |
Db     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120

Qy    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
      |
Db    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
      |
Db    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241 GINNNRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300
      |
Db    241 GINNNRIDLRSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300

Qy    301 EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTTVGELSRLVSEARNLLEVSEVEQELACQ 360
      |
Db    301 EQQKLESIAADMKAFVENYPQFKKMSGTVSKHVTTVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy    361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
      |
Db    361 NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420

Qy    421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK 480
      |
Db    421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK 480

Qy    481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRRTTPGVRIVLGGTTVHNT 540
      |
Db    481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRRTTPGVRIVLGGTTVHNT 540

Qy    541 KSFL EEVLASGLHSRSKESQVTSRS 566
      |
Db    541 K----RALKSHQGQRAEDET VVGGRA 562
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RESULT 13

US-11-443-428A-738992

; Sequence 738992, Application US/11443428A

; Patent No. 7745391

; GENERAL INFORMATION:

```
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738992
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738992
```

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Query Match          93.9%; Score 2721; DB 3; Length 534;
Best Local Similarity 100.0%;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      37 MVYTQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI 96
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MVYTQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI 60

Qy      97 YFSNVISKSDVKSLAEADEQEVVAEVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLS 156
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 YFSNVISKSDVKSLAEADEQEVVAEVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLS 120

Qy     157 RTTQGLTALLLSLKKCPMIRYQLSSEAAKRLAECVKQVITKEYELFEFRRTTEVPPLLLIL 216
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 RTTQGLTALLLSLKKCPMIRYQLSSEAAKRLAECVKQVITKEYELFEFRRTTEVPPLLLIL 180

Qy     217 DRCDDAITPLLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNM 276
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 DRCDDAITPLLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNM 240

Qy     277 YLNFAEIGSNIKNLMEDFQKKKPKEQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVG 336
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 YLNFAEIGSNIKNLMEDFQKKKPKEQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVG 300

Qy     337 ELSRLVSEARNLLEVSEVEQELACQNDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYE 396
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 ELSRLVSEARNLLEVSEVEQELACQNDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYE 360

Qy     397 RHSSNSLPGLMMDLRNKGVSEKYRKLVS AVVEYGGKRVGSDLFSPKDAVAITKQFLKGL 456
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 RHSSNSLPGLMMDLRNKGVSEKYRKLVS AVVEYGGKRVGSDLFSPKDAVAITKQFLKGL 420

Qy     457 KGVENVYTQHQPFLHETLDHLIKGRLENLYPYLGPSTLRDRPQDIIVFVIGGATYEEAL 516
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 KGVENVYTQHQPFLHETLDHLIKGRLENLYPYLGPSTLRDRPQDIIVFVIGGATYEEAL 480

Qy     517 TVYNLNRTTPGVRIVLGGTTVHNTKSFLEEVLASGLHSRSKESQVTSRSASRR 570
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 TVYNLNRTTPGVRIVLGGTTVHNTKSFLEEVLASGLHSRSKESQVTSRSASRR 534
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RESULT 14
US-11-443-428A-739001
; Sequence 739001, Application US/11443428A
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```
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 739001
; LENGTH: 534
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-739001
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Query Match          93.9%; Score 2721; DB 3; Length 534;
Best Local Similarity 100.0%;
Matches 534; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      37 MVTQTQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI 96
          |||
Db      1 MVTQTQSEILQKEVYLFERIDSQNREIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFI 60

Qy      97 YFSNVISKSDVKSLAEADEQEVAEVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLS 156
          |||
Db      61 YFSNVISKSDVKSLAEADEQEVAEVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLS 120

Qy     157 RTTQGLTALLLSLKKCPMIRYQLSSEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLIL 216
          |||
Db     121 RTTQGLTALLLSLKKCPMIRYQLSSEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLIL 180

Qy     217 DRCDDAITPLLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNM 276
          |||
Db     181 DRCDDAITPLLNQWTYQAMVHELLGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNM 240

Qy     277 YLNFAEIGSNIKNLMEDFQKKKPKEQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVG 336
          |||
Db     241 YLNFAEIGSNIKNLMEDFQKKKPKEQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVG 300

Qy     337 ELSRLVSEARNLLEVSEVEQELACQNDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYE 396
          |||
Db     301 ELSRLVSEARNLLEVSEVEQELACQNDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYE 360

Qy     397 RHSSNSLPGLMMDLRNKGVSEKYRKLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGL 456
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Db     361 RHSSNSLPGLMMDLRNKGVSEKYRKLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGL 420

Qy     457 KGVENVYTQHQPFLHETLDHLIKGRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEAL 516
          |||
Db     421 KGVENVYTQHQPFLHETLDHLIKGRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEAL 480

Qy     517 TVYNLNRTPGVRIVLGGTTVHNTKSFLEEVLASGLHSRSKESQVTSRSASRR 570
          |||
Db     481 TVYNLNRTPGVRIVLGGTTVHNTKSFLEEVLASGLHSRSKESQVTSRSASRR 534
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RESULT 15

US-11-443-428A-739004
; Sequence 739004, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 739004
; LENGTH: 526
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-739004

Query Match 88.0%; Score 2550; DB 3; Length 526;
Best Local Similarity 100.0%;
Matches 499; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRP	499
Db	481	RLKENLYPYLGPSTLRDRP	499

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SCORE 3.0

SCORE Search Results Details for Application 09556178 and Search Result 20101203_114248_us-09-556-178-1.rapbm.

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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:43:00 ; Search time 201 Seconds
(without alignments)
3841.159 Million cell updates/sec

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6210261 seqs, 1354514112 residues

Total number of hits satisfying chosen parameters: 6210261

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /ABSS/Data/CRF/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /ABSS/Data/CRF/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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5: /ABSS/Data/CRF/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /ABSS/Data/CRF/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*
7: /ABSS/Data/CRF/ptodata/1/pubpaa/US11B_PUBCOMB.pep:*
8: /ABSS/Data/CRF/ptodata/1/pubpaa/US12_PUBCOMB.pep:*
SUMMARIES

		%				
		Query				
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1	2898	100.0	570	4	US-10-788-792-187	Sequence 187, App
2	2898	100.0	570	5	US-10-511-937-2612	Sequence 2612, Ap
3	2898	100.0	570	5	US-10-219-051B-7142	Sequence 7142, Ap
4	2898	100.0	570	5	US-10-917-503-15151	Sequence 15151, A
5	2898	100.0	570	6	US-11-371-354-75315	Sequence 75315, A
6	2898	100.0	570	6	US-11-443-428A-738990	Sequence 738990,
7	2898	100.0	570	6	US-11-443-428A-738993	Sequence 738993,
8	2898	100.0	570	6	US-11-443-428A-738994	Sequence 738994,
9	2898	100.0	570	6	US-11-443-428A-739003	Sequence 739003,

10	2898	100.0	570	7	US-11-706-155-684	Sequence 684, App
11	2898	100.0	570	8	US-12-584-615-2612	Sequence 2612, Ap
12	2840	98.0	570	5	US-10-219-051B-7140	Sequence 7140, Ap
13	2815.5	97.2	578	5	US-10-450-763-34837	Sequence 34837, A
14	2783	96.0	552	6	US-11-443-428A-738991	Sequence 738991,
15	2777	95.8	552	6	US-11-443-428A-738998	Sequence 738998,
16	2769	95.5	612	6	US-11-443-428A-739002	Sequence 739002,
17	2721	93.9	534	6	US-11-443-428A-738992	Sequence 738992,
18	2721	93.9	534	6	US-11-443-428A-739001	Sequence 739001,
19	2550	88.0	526	6	US-11-443-428A-739004	Sequence 739004,
20	1873	64.6	372	6	US-11-443-428A-738999	Sequence 738999,
21	1755	60.6	359	6	US-11-443-428A-738995	Sequence 738995,
22	1584	54.7	574	6	US-11-097-143-18048	Sequence 18048, A
23	1310	45.2	441	5	US-10-450-763-34838	Sequence 34838, A
24	1299.5	44.8	567	5	US-10-449-902-43905	Sequence 43905, A
25	1286	44.4	568	4	US-10-437-963-112637	Sequence 112637,
26	1286	44.4	568	5	US-10-437-963-112637	Sequence 112637,
27	1273	43.9	567	6	US-11-241-607-62939	Sequence 62939, A
28	1273	43.9	567	8	US-12-435-281-62939	Sequence 62939, A
29	1270	43.8	567	8	US-12-286-964-7714	Sequence 7714, Ap
30	1089	37.6	567	4	US-10-425-115-238853	Sequence 238853,
31	1089	37.6	567	5	US-10-425-115-238853	Sequence 238853,
32	1030.5	35.6	212	4	US-10-425-115-348394	Sequence 348394,
33	1030.5	35.6	212	5	US-10-425-115-348394	Sequence 348394,
34	976	33.7	577	3	US-09-801-368-420	Sequence 420, App
35	976	33.7	577	3	US-09-800-863-420	Sequence 420, App
36	976	33.7	577	5	US-10-309-407-420	Sequence 420, App
37	917	31.6	398	5	US-10-703-032-125739	Sequence 125739,
38	788	27.2	162	6	US-11-443-428A-739006	Sequence 739006,
39	757.5	26.1	200	6	US-11-443-428A-738996	Sequence 738996,
40	753	26.0	364	5	US-10-449-902-35619	Sequence 35619, A
41	744	25.7	158	6	US-11-443-428A-739005	Sequence 739005,
42	671.5	23.2	303	4	US-10-425-115-238857	Sequence 238857,
43	671.5	23.2	303	5	US-10-425-115-238857	Sequence 238857,
44	613	21.2	129	6	US-11-443-428A-739000	Sequence 739000,
45	574	19.8	219	7	US-11-360-355-123305	Sequence 123305,

ALIGNMENTS

RESULT 1

US-10-788-792-187
 ; Sequence 187, Application US/10788792
 ; Publication No. US20040191819A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayer Pharmaceuticals Corporation
 ; APPLICANT: Eveleigh, Deepa
 ; APPLICANT: Bigwood, Douglas
 ; TITLE OF INVENTION: EXPRESSION PROFILES FOR BREAST CANCER AND METHODS OF USE
 ; FILE REFERENCE: 5152
 ; CURRENT APPLICATION NUMBER: US/10/788,792
 ; CURRENT FILING DATE: 2004-02-27
 ; PRIOR APPLICATION NUMBER: US 60/450,655
 ; PRIOR FILING DATE: 2003-02-28
 ; NUMBER OF SEQ ID NOS: 254
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 187
 ; LENGTH: 570
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-788-792-187

Query Match 100.0%; Score 2898; DB 4; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKA FVENYPQFKMSGTVSKHVT VVGELSRLVSE RNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKA FVENYPQFKMSGTVSKHVT VVGELSRLVSE RNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKG VSEKYR	420
Db	361	NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKG VSEKYR	420
Qy	421	KLVS AVVEYGGKRV RGSDFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDH LIKG	480
Db	421	KLVS AVVEYGGKRV RGSDFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDH LIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEV LASGLHSRSKES SQVTSRSASRR	570
Db	541	KSFLEEV LASGLHSRSKES SQVTSRSASRR	570

RESULT 2

US-10-511-937-2612

; Sequence 2612, Application US/10511937

; Publication No. US20060088836A1

; GENERAL INFORMATION:

; APPLICANT: EXPRESSION DIAGNOSTICS, INC.

; APPLICANT: Wohlgemuth, Jay

; APPLICANT: Fry, Kirk

; APPLICANT: Woodward, Robert

; APPLICANT: Ly, Ngoc

; APPLICANT: Prentice, James

; APPLICANT: Morris, MacDonald

; APPLICANT: Rosenberg, Steven

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION

; FILE REFERENCE: 506612000104

; CURRENT APPLICATION NUMBER: US/10/511,937

; CURRENT FILING DATE: 2004-10-19

; PRIOR APPLICATION NUMBER: PCT/US2003/012946

; PRIOR FILING DATE: 2003-04-24

; PRIOR APPLICATION NUMBER: US 10/131,831

; PRIOR FILING DATE: 2002-04-24

; PRIOR APPLICATION NUMBER: US 10/325,899

; PRIOR FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 3117

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2612
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-511-937-2612

Query Match 100.0%; Score 2898; DB 5; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVLVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVLVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 3

US-10-219-051B-7142

; Sequence 7142, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347

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; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 7142
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Refseq / NP_009189
; DATABASE ENTRY DATE: 2002-11-04
US-10-219-051B-7142
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Query Match          100.0%; Score 2898; DB 5; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MNVVFVAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120

Qy    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK 300

Qy    301 EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy    361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420

Qy    421 KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK 480

Qy    481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy    541 KSFLEEVLASGLHSRSKESQVTSRSASRR 570
        ||||||||||||||||||||||||||||
Db    541 KSFLEEVLASGLHSRSKESQVTSRSASRR 570
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RESULT 4
US-10-917-503-15151
; Sequence 15151, Application US/10917503
; Publication No. US20070105122A1
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
```

```
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15151
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503-15151
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Query Match          100.0%; Score 2898; DB 5; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MNVVFHAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR 60
        |
Db      1 MNVVFHAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
        |
Db     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120

Qy    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
        |
Db    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy    181 SEAAKRLAECVKQVITKEYELFEFRRTTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240
        |
Db    181 SEAAKRLAECVKQVITKEYELFEFRRTTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL 240

Qy    241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK 300
        |
Db    241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK 300

Qy    301 EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
        |
Db    301 EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy    361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
        |
Db    361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420

Qy    421 KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK 480
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Db          421  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
KLVS AVVEYGGKRV RGS DLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDH LIKG 480

Qy          481  RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540
|||||
Db          481  RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT 540

Qy          541  KS FLEEV LASGLHSRSKES SQVTSRSASRR 570
|||||
Db          541  KS FLEEV LASGLHSRSKES SQVTSRSASRR 570
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RESULT 5

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US-11-371-354-75315
; Sequence 75315, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
; APPLICANT: LIANG, FENG
; TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
; TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
; FILE REFERENCE: INV-1005-UT2
; CURRENT APPLICATION NUMBER: US/11/371,354
; CURRENT FILING DATE: 2006-03-07
; PRIOR APPLICATION NUMBER: 60/673,045
; PRIOR FILING DATE: 2005-04-19
; PRIOR APPLICATION NUMBER: 60/665,199
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/665,200
; PRIOR FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/659,493
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/659,492
; PRIOR FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/953,586
; PRIOR FILING DATE: 2005-02-15
; PRIOR APPLICATION NUMBER: 60/651,390
; PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75315
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-371-354-75315
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Query Match          100.0%; Score 2898; DB 6; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy          1  MNVVF AVKQYISKMIEDSGPGMKVLLMDKET TGIVSMVYTQSEILQKEVYLFERIDSQNR 60
|||||
Db          1  MNVVF AVKQYISKMIEDSGPGMKVLLMDKET TGIVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy          61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQE VVA 120
|||||
Db          61  EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQE VVA 120

Qy          121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
|||||
Db          121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy          181 SEAAKRLAE CVKQVITKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQW TYQAMVHELL 240
|||||
Db          181 SEAAKRLAE CVKQVITKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQW TYQAMVHELL 240

Qy          241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK 300
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Db	241		GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ		360
Db	301		EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR		420
Db	361		NDHSSALQNIKRLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK		480
Db	421		KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT		540
Db	481		RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR		570
Db	541		KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 6

US-11-443-428A-738990
; Sequence 738990, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738990
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738990

Query Match 100.0%; Score 2898; DB 6; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1		MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIIVSMVYTQSEILQKEVYLFERIDSQNR 60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61		EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121		EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS 180

Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 7

US-11-443-428A-738993
; Sequence 738993, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738993
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738993

Query Match 100.0%; Score 2898; DB 6; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120

Db	61	 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	 SEAAKRLAECVKQVITKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKA FVENYPQFKKMSGTVSKHVT VVGELSRLVSERN LLEVSEVEQELACQ	360
Db	301	 EQQKLESIADMKA FVENYPQFKKMSGTVSKHVT VVGELSRLVSERN LLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKG VSEKYR	420
Db	361	 NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKG VSEKYR	420
Qy	421	KLVS AVVEYGGKRV RGS DLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDH LIKG	480
Db	421	 KLVS AVVEYGGKRV RGS DLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDH LIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNR TTPGVRIVLGGTTVHNT	540
Db	481	 RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNR TTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKES SQVTSRSASRR	570
Db	541	 KSFLEEVLASGLHSRSKES SQVTSRSASRR	570

RESULT 8

US-11-443-428A-738994

; Sequence 738994, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 738994

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-443-428A-738994

Query Match 100.0%; Score 2898; DB 6; Length 570;
 Best Local Similarity 100.0%;
 Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHЛИK	480
Db	421	KLVSAVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHЛИK	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570

RESULT 9

US-11-443-428A-739003

; Sequence 739003, Application US/11443428A

; Publication No. US20070083334A1

; GENERAL INFORMATION:

; APPLICANT: Mintz, Liat

; APPLICANT: Xie, Hanqing

; APPLICANT: Dahari, Dvir

; APPLICANT: Levanon, Erez

; APPLICANT: Freilich, Shiri

; APPLICANT: Beck, Nili

; APPLICANT: Zhu, Wei-Yong

; APPLICANT: Wasserman, Alon

; APPLICANT: Hermesh, Chen

; APPLICANT: Azar, Idit

; APPLICANT: Bernstein, Jeanne

; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES

; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 739003

; LENGTH: 570

; TYPE: PRT

; ORGANISM: Homo sapiens
US-11-443-428A-739003

Query Match 100.0%; Score 2898; DB 6; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFR RTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKA FVENYPQFKKMSGTVSKHVT VVGELSRLVSE RN LLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKA FVENYPQFKKMSGTVSKHVT VVGELSRLVSE RN LLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKG VSEKYR	420
Db	361	NDHSSALQNIKRL LQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKG VSEKYR	420
Qy	421	KLVS AVVEYGGKRV RGS DLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDH LIKG	480
Db	421	KLVS AVVEYGGKRV RGS DLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDH LIKG	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEV LASGLHSRSKES SQVTSRSASRR	570
Db	541	KSFLEEV LASGLHSRSKES SQVTSRSASRR	570

RESULT 10

US-11-706-155-684

; Sequence 684, Application US/11706155

; Publication No. US20080075722A1

; GENERAL INFORMATION

; APPLICANT: DEPINHO, RONALD A.

; APPLICANT: ANDERSON, KENNETH C.

; APPLICANT: CARRASCO, DANIEL R.

; APPLICANT: TONON, GIOVANNI

; APPLICANT: BRENNAN, CAMERON

; APPLICANT: SHAUGHNESSY, JOHN D., Jr.

; APPLICANT: CHIN, LYND A

; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,

; TITLE OF INVENTION: PREVENTION, AND THERAPY OF CANCER

; FILE REFERENCE: DFS-065.01

; CURRENT APPLICATION NUMBER: US/11/706,155

; CURRENT FILING DATE: 2007-11-09

; PRIOR APPLICATION NUMBER: 60/773,072

; PRIOR FILING DATE: 2006-02-14

; NUMBER OF SEQ ID NOS: 713
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 684
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-706-155-684

Query Match 100.0%; Score 2898; DB 7; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLQNPVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSSEKYR	420
Db	361	NDHSSALQNIKRLQLQNPVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570

RESULT 11

US-12-584-615-2612

; Sequence 2612, Application US/12584615
; Publication No. US20100151467A1
; GENERAL INFORMATION
; APPLICANT: XDx, INC.
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; APPLICANT: Prentice, James
; APPLICANT: Morris, MacDonald
; APPLICANT: Rosenberg, Steven
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING

; TITLE OF INVENTION:AND MONITORING TRANSPLANT REJECTION
; FILE REFERENCE: 506612000123
; CURRENT APPLICATION NUMBER: US/12/584,615
; CURRENT FILING DATE: 2009-09-23
; PRIOR APPLICATION NUMBER: US 10/511,937
; PRIOR FILING DATE: 2005-07-22
; PRIOR APPLICATION NUMBER: PCT/US2003/12946
; PRIOR FILING DATE: 2003-04-24
; PRIOR APPLICATION NUMBER: US 10/325,899
; PRIOR FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: US 10/131,831
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 13083
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2612
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Homo sapiens
US-12-584-615-2612

Query Match 100.0%; Score 2898; DB 8; Length 570;
Best Local Similarity 100.0%;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFVENYPQFKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLQLQNPVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLQLQNPVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	541	KSFLEEVLASGLHSRSKESSQVTSRSASRR	570

RESULT 12
US-10-219-051B-7140

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; Sequence 7140, Application US/10219051B
; Publication No. US20070015145A1
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation doing business as Massachusetts General
; APPLICANT: Hospital / Bayer AG
; TITLE OF INVENTION: Nucleotide sequences involved in pain
; FILE REFERENCE: LeA 35693 Foreign Countries
; CURRENT APPLICATION NUMBER: US/10/219,051B
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US 60/312,147
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: US 60/346,382
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/333,347
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 14715
; SOFTWARE: Perl script
; SEQ ID NO 7140
; LENGTH: 570
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: SWISS-Prot / AAB53041
; DATABASE ENTRY DATE: 2002-06-15
US-10-219-051B-7140
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Query Match          98.0%; Score 2840; DB 5; Length 570;
Best Local Similarity 97.2%;
Matches 554; Conservative 12; Mismatches 4; Indels 0; Gaps 0;
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Qy      1 MNVVFQVQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60
        |
Db      1 MNVVFQVQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR 60

Qy     61 EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA 120
        |
Db     61 EIMKHLKAICFLRPTKENVDSLIQELRRPKYSIYFIYFSNVISKSDVKSLAEADEQEVVA 120

Qy    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180
        |
Db    121 EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS 180

Qy    181 SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWQTYQAMVHELL 240
        |
Db    181 SEAAKRLGECVKQVISKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWQTYQAMVHELL 240

Qy    241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKKPK 300
        |
Db    241 GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNF AEIGSNIKNLMEDFQKKRPK 300

Qy    301 EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360
        |
Db    301 EQQKLESIAADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ 360

Qy    361 NDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR 420
        |
Db    361 NDHSSALQNVKRLQLNPKVTEFDAVRLVMLYALHYERHSSNSLPGLIVDLRSKGVAEKYR 420

Qy    421 KLVSQVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLLIKG 480
        |
Db    421 KLVSQVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLLIKG 480

Qy    481 RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTIVHNT 540
        |
Db    481 RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTIHNT 540

Qy    541 KSFLLEEVLASGLHSRSKESQVTSRSASRR 570
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|||||:|||||
Db 541 KSFLEEVLASGLHSRSRESSQATSRASRR 570

RESULT 13

US-10-450-763-34837
; Sequence 34837, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 34837
; LENGTH: 578
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (218)..(258)
; OTHER INFORMATION: Sec1 family domain identified by eMATRIX, accession number
; OTHER INFORMATION: PF00995B, p-value=6.745e-25, raw score of 17.37
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: (95)..(562)
; OTHER INFORMATION: Sec1 family domain identified by PFam, accession name Sec1, E
; OTHER INFORMATION: -value=2.9e-164, PFam score of 559.1
US-10-450-763-34837

Query Match 97.2%; Score 2815.5; DB 5; Length 578;
Best Local Similarity 97.7%;
Matches 558; Conservative 3; Mismatches 9; Indels 1; Gaps 1;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	8	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	67
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLA-EADEQEVV	119
Db	68	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVEVIGLKLIEQEVV	127
Qy	120	AEVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQL	179
Db	128	AEVQEFYGDYIAVNPFLFSLNILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQL	187
Qy	180	SSEAAKRLAECVKQVITKEYELFEFRRTVPPLLLILDRCDDAITPLLNQWTYQAMVHEL	239
Db	188	SSEAAKRLAECVKQVITKEYELFEFRRTVPPLLLILDRLDDAITPLLNQWTYQAMVHEL	247
Qy	240	LGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKP	299
Db	248	LGINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKP	307
Qy	300	KEQQKLESIA DMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELAC	359
Db	308	KEQQKLESIGSMKAFVENYPQFKKMSGTVSKHVTVVGELSRLVSERNLLLEVSEVEQELAC	367
Qy	360	QNDHSSALQNIKRLQLNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKY	419

Db	368	QNDHSSALQNIKRLQLQPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKY	427
Qy	420	RKLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	479
Db	428	RKLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVGNVYTQLQPFLHETLDHLIK	487
Qy	480	GRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGTTVHN	539
Db	488	GRLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGTTVHN	547
Qy	540	TKSFLEEVLASGLHSRSKESSQVTSRSASRR	570
Db	548	TKSFLEEVLASGLHSRSKESSQVTSRSASRR	578

RESULT 14

US-11-443-428A-738991
; Sequence 738991, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738991
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-738991

Query Match 96.0%; Score 2783; DB 6; Length 552;
Best Local Similarity 96.8%;
Matches 552; Conservative 0; Mismatches 0; Indels 18; Gaps 1;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGVSMVYTQSEILQKEVYLFERIDSQ--	58
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	59	-----ENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	102
Qy	121	EVQEFYGDYIAVNPHLFSNLIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	180
Db	103	EVQEFYGDYIAVNPHLFSNLIGCCQGRNWDPAQLSRTTQGLTALLSLKKCPMIRYQLS	162
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Db	163	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	222
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	223	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	282

Qy	301	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVVGELSRLVSEERNLLEVSEVEQELACQ	360
Db	283	EQQKLESIADMKAFVENYPQFKKMSGTVSKHVTTVVGELSRLVSEERNLLEVSEVEQELACQ	342
Qy	361	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	343	NDHSSALQNIKRLQLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	402
Qy	421	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	403	KLVS AVVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	462
Qy	481	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	463	RLKENLYPYLGPSTLDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	522
Qy	541	KSFLEEVLASGLHSRSKESQVTSRSASRR	570
Db	523	KSFLEEVLASGLHSRSKESQVTSRSASRR	552

RESULT 15
 US-11-443-428A-738998
 ; Sequence 738998, Application US/11443428A
 ; Publication No. US20070083334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mintz, Liat
 ; APPLICANT: Xie, Hanqing
 ; APPLICANT: Dahari, Dvir
 ; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
 ; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
 ; APPLICANT: Hermesh, Chen
 ; APPLICANT: Azar, Idit
 ; APPLICANT: Bernstein, Jeanne
 ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
 ; FILE REFERENCE: 02/23929
 ; CURRENT APPLICATION NUMBER: US/11/443,428A
 ; CURRENT FILING DATE: 2006-05-31
 ; NUMBER OF SEQ ID NOS: 1034312
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 738998
 ; LENGTH: 552
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-443-428A-738998

Query Match 95.8%; Score 2777; DB 6; Length 552;
 Best Local Similarity 99.3%;
 Matches 547; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Db	1	MNVVFAVKQYISKMIEDSGPGMKVLLMDKETTGIVSMVYTQSEILQKEVYLFERIDSQNR	60
Qy	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Db	61	EIMKHLKAICFLRPTKENVDYIIQELRRPKYTIYFIYFSNVISKSDVKSLAEADEQEVVA	120
Qy	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Db	121	EVQEFYGDYIAVNPHLFSNLILGCCQGRNWDPAQLSRTTQGLTALLLSLKKCPMIRYQLS	180
Qy	181	SEAAKRLAECVKQVITKEYELFEFRRTVEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240

Db	181	SEAAKRLAECVKQVITKEYELFEFRRTEVPPLLLILDRCDDAITPLLNQWTYQAMVHELL	240
Qy	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Db	241	GINNNRIDLSRVPGISKDLREVVLSAENDEFYANNMYLNFAEIGSNIKNLMEDFQKKKPK	300
Qy	301	EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Db	301	EQQKLESIADMKAFFVENYPQFKKMSGTVSKHVTVVGELSRLVSEARNLLEVSEVEQELACQ	360
Qy	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Db	361	NDHSSALQNIKRLLQNPKVTEFDAARLVMLYALHYERHSSNSLPGLMMDLRNKGVSEKYR	420
Qy	421	KLVSATVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Db	421	KLVSATVEYGGKRVRGSDLFSPKDAVAITKQFLKGLKGVENVYTQHQPFLHETLDHLIK	480
Qy	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Db	481	RLKENLYPYLGPSTLRDRPQDIIVFVIGGATYEEALTVYNLNRTPGVRIVLGGTTVHNT	540
Qy	541	KS--FLEEVLA	549
Db	541	KSKRFLREGLA	551

Search completed: December 3, 2010, 11:46:57
Job time : 237 secs

SCORE 3.0

SCORE Search Results Details for Application 09556178 and Search Result 20101203_114249_us-09-556-178-1.rapbn.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101203_114249_us-09-556-178-1.rapbn.

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OM protein - protein search, using sw model

Run on: December 3, 2010, 11:42:55 ; Search time 5 Seconds
(without alignments)
160.331 Million cell updates/sec

Title: US-09-556-178-1
Perfect score: 2898
Sequence: 1 MNVVFVAVKQYISKMIEDSGP.....GLHSRSKESQVTSRSASRR 570

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 14841 seqs, 1406414 residues

Total number of hits satisfying chosen parameters: 14841

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /ABSS/Data/CRF/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
2: /ABSS/Data/CRF/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
3: /ABSS/Data/CRF/ptodata/1/pubpaa/US12_NEW_PUB.pep:*
SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	123.5	4.3	980	3	US-12-293-792A-10	Sequence 10, Appl	
2	117	4.0	500	3	US-12-441-092-4	Sequence 4, Appli	
3	117	4.0	667	3	US-12-441-092-2	Sequence 2, Appli	
4	114	3.9	1977	3	US-12-739-689-45	Sequence 45, Appl	
5	114	3.9	1977	3	US-12-739-723-39	Sequence 39, Appl	
6	113	3.9	1396	3	US-12-086-571-50	Sequence 50, Appl	
7	109	3.8	488	3	US-12-086-571-175	Sequence 175, App	
8	107.5	3.7	813	3	US-12-739-689-36	Sequence 36, Appl	
9	107.5	3.7	2325	3	US-12-739-689-28	Sequence 28, Appl	
10	107.5	3.7	2325	3	US-12-739-723-30	Sequence 30, Appl	
11	99.5	3.4	2757	3	US-12-625-053A-38	Sequence 38, Appl	
12	99	3.4	755	3	US-12-345-877-181	Sequence 181, App	
13	97.5	3.4	1960	3	US-12-864-218-90	Sequence 90, Appl	
14	96.5	3.3	483	3	US-12-441-092-41	Sequence 41, Appl	

15	96.5	3.3	1979	3	US-12-739-689-47	Sequence 47, Appl
16	96.5	3.3	1979	3	US-12-739-723-41	Sequence 41, Appl
17	96	3.3	3692	3	US-12-625-053A-48	Sequence 48, Appl
18	95.5	3.3	1014	3	US-12-345-877-251	Sequence 251, App
19	95	3.3	334	3	US-12-441-092-8	Sequence 8, Appli
20	95	3.3	501	3	US-12-441-092-6	Sequence 6, Appli
21	94	3.2	787	3	US-12-739-689-54	Sequence 54, Appl
22	94	3.2	808	3	US-12-523-023-3	Sequence 3, Appli
23	93.5	3.2	534	3	US-12-764-333A-3	Sequence 3, Appli
24	93.5	3.2	794	3	US-12-523-023-4	Sequence 4, Appli
25	92	3.2	878	3	US-12-733-159A-166	Sequence 166, App
26	91.5	3.2	788	3	US-12-739-689-55	Sequence 55, Appl
27	90.5	3.1	408	3	US-12-441-092-43	Sequence 43, Appl
28	90.5	3.1	872	3	US-12-523-023-1	Sequence 1, Appli
29	88	3.0	303	3	US-12-441-092-40	Sequence 40, Appl
30	88	3.0	332	3	US-12-441-092-39	Sequence 39, Appl
31	88	3.0	2005	3	US-12-317-496-34	Sequence 34, Appl
32	87.5	3.0	913	3	US-12-086-571-250	Sequence 250, App
33	87.5	3.0	1757	3	US-12-787-298-15	Sequence 15, Appl
34	87	3.0	295	3	US-12-625-053A-50	Sequence 50, Appl
35	87	3.0	562	3	US-12-086-571-242	Sequence 242, App
36	87	3.0	2005	3	US-12-317-496-35	Sequence 35, Appl
37	87	3.0	2339	3	US-12-739-689-26	Sequence 26, Appl
38	87	3.0	2339	3	US-12-739-723-26	Sequence 26, Appl
39	87	3.0	2589	3	US-12-739-689-42	Sequence 42, Appl
40	87	3.0	2589	3	US-12-739-723-28	Sequence 28, Appl
41	85.5	3.0	801	3	US-12-784-310-2	Sequence 2, Appli
42	85	2.9	858	3	US-12-682-544-14	Sequence 14, Appl
43	85	2.9	858	3	US-12-682-544-15	Sequence 15, Appl
44	85	2.9	858	3	US-12-682-544-16	Sequence 16, Appl
45	84.5	2.9	530	3	US-12-784-310-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1

US-12-293-792A-10

; Sequence 10, Application US/12293792A

; Publication No. US20100297178A1

; GENERAL INFORMATION

; APPLICANT: Murdoch University

; TITLE OF INVENTION: Novel Genes and Proteins of Brachyspira hyodysenteriae and Use of

; TITLE OF INVENTION: Same for Diagnosis and Therapy

; FILE REFERENCE: P78788.US

; CURRENT APPLICATION NUMBER: US/12/293,792A

; CURRENT FILING DATE: 2010-07-15

; NUMBER OF SEQ ID NOS: 56

; SOFTWARE: PatentIn version 3.5

; SEQ ID NO 10

; LENGTH: 980

; TYPE: PRT

; ORGANISM: Brachyspira hyodysenteriae

US-12-293-792A-10

Query Match 4.3%; Score 123.5; DB 3; Length 980;

Best Local Similarity 18.2%;

Matches 124; Conservative 106; Mismatches 262; Indels 191; Gaps 26;

Qy	5	FAVKQYISKMIED-----SGPGMKVLLMDKETTGVSMVYTQSEI-----	44
		: : :: : : : : :	
Db	228	FAIVDEVDSILIDEARTPLIISGPAEKNIKMYEIDRIIPML-KQAEVDERMREVAGTGD	286
Qy	45	-----LQKEVYLFER-----IDSQNREIMKHL-KAICFLRPTKENVDYIIQ	84
		: : : : : : : : :	
Db	287	YVLDEKDKNVYLTTEEGVHKVEKLLNVENLYGAQSSTIVHHVNQALKAHKVFKKDVDYDMVT	346